ORIGIN

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Search completed: February 20, 2004, 01:41:36 Job time : 137.422 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (bordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Akahira,S., Akiyama,J., Arakawa,T.,

Romo,H., Alzawa,K., Akahira,S., Akiyama,J., Arakawa,T.,

Romo,H., Alzawa,K., Tehii,Y., Ishikawa,T., Itch,M.,

Hirozane,T., Hori, F., Tehii,Y., Ishikawa,J., Ishikawa,T., Itch,M.,

Hirozane,T., Hori, F., Tehii,Y., Ishikawa,J., Ishikawa,T., Itch,M.,

Kiyosawa,H., Kadola,K., Kagawa,J., Kai,C., Kawi,J., Kikuchi,N.,

Kiyosawa,H., Kojima,Y., Komo,S., Koya,S., Kurihara,C., Kuchina,C.,

Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,

Okazak,I., Ono,T., Owa,C., Saito,H., Sakai,C., Sano,K.,

Solabet,Y., Subhata,Y., Suzuki,H., Tagawa,A., Shiraki,T.,

Romana,K., Yoshida,K., Yoshiki,A., Yoshida,A., Yokota, Y., Watahiki,A.,

Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muzamatsu,M. and

Haysahizak,Y.

RIKEN Mouse ESTS (Konno,H., et al.)

Nupublished (2000)

Al. Oppidiablished Hayahizaki,

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC) Yokohama Institute

Contextory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC) Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehino-2022 Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-922

Fax: 81-45-503-922

Fax: 81-45-503-922

Fax: 81-45-503-922

Fax: 18-45-503-922

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                                                                                                          /organism="Oncorhynchus mykiss"
/mol type="mRNA"
/strain="Karl Vierke"
/db xref="taxarl Vierke"
/clone lib="Oncorhynchus mykiss reproductive"
/note="Vector: portytopo, Library Creator: Kristian R von
Schalburg; Rainbow trout tissue contributors: Mountain
Trout Sales (Sooke, B.C.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB306076 RIKEN full-length enriched, adult male corpora quadrigemina Mus musculus cDNA clone B230206M01 3', mRNA sequence. BB306076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       11arity 90.0%; Pred. No. 2.2e+03; Conservative 0; Mismatches 2;
bioinformatics: Gordon D Brown
                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGGACAGGTTAGGGCTTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crecacercaceacrire 92
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conservat
                                POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB306076
                                                          FEATURES
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/tissue_type="corpora quadrigemina"
dev stage="adult"
lab_host="DHIOB"
/clone_lib="RIKEN full-length enriched, adult male corpora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                      /note==Site 1: Sall; Site 2: BamHI; cDNA library was /note==Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGAGCATCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%; Score 16.8; DB 10;
90.0%; Pred. No. 2.2e+03;
tive 0; Mismatches 2;
                                                                                           'organism="Mus musculus"
                                                                                                             /mol_type="mRNA"
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/clone="B230206M01"
                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CIGGACAGGITAGGGCTITG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 crrcacacerrarecerrie 91
                                                                                                                                                                                                                                                                                          quadrigemina"
                                                                                                                                                                               sex="male"
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us-09-939-853a-140.rni

Sequence 2591. Apple Sequence 84. Appl Sequence 1350, Apple Sequence 5. Appli Sequence 5. Appli Sequence 122, Appli Sequence 112, Appli Sequence 17, Appli Sequence 47, Appli Sequence 47, Appli Sequence 69, Appli Sequence 6

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APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PELING DATE: 2000-01-27
CURRENT FLING DATE: US/09/489,039A
CURRENT FLING DATE: US 60/117,747
PRIOR PAPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
SEQ ID NOS: 14342
SEQ ID NOS: 14342
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-09-816-095-3
; Sequence 3, Application US/09816095
; Patent No. 6664084
; Fatent No. 6664084
; GENERAL INFORMATION:
APPLICANT: GAN, Weiniu
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS,
CURRENT FALLING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 5
; SETWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 99916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 99916;
US-09-404-641-80
US-09-416-69
US-09-328-352-2591
US-09-620-312D-886
US-09-134-000C-1350
US-09-784-85-5
US-09-784-85-5
US-09-784-859-5
US-09-784-859-5
US-09-784-859-5
US-09-312D-863
US-09-21-731A-122
4 US-08-916-421B-1
4 US-08-916-421B-1
US-09-329-911A-47
US-09-229-911A-47
US-09-229-911A-69
US-09-229-911A-69
US-09-229-911A-69
US-09-229-911A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%; Score 15.8; D 89.5%; Pred. No. 86; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-489-039A-4299/c
; Sequence 4299, Application US/09489039A
; Ratent No. 6610836
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5532 İdGACAGAİİAGGCCİİİĞ 5550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURE:
NAME/KEY:
LOCATION: (1)...(99916)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGGACAGGTTAGGGCTTTG 20
                                    1398
1572
1735
1773
1799
1799
1719
41171
1664976
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Matches 17; Conserv
                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-816-095-3
     Query Match
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                                                                                                                  February 19, 2004, 21:32:00 ; Search time 3.2454 Seconds (without alignments) 3419.919 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, App
Sequence 57, At
Sequence 4, App
Sequence 4, App
Sequence 2, App
Sequence 2, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents NA:*

1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

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6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-489-039A-4299
US-09-071-035-431
US-09-134-000C-3193
US-09-134-000C-3193
US-09-620-312D-925
US-09-620-312D-925
US-08-920-4221-1
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US-08-486-855A-1
US-08-486-855A-1
US-08-486-855A-1
US-08-486-855A-1
US-08-486-855A-1
US-08-486-855A-1
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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US-09-671-317-191
                                                                                                                                                                                                                                                                                                            682709 segs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      using sw model
                                                                                                                                                                                                                             1 ctggacaggttagggctttg 20
                                                                                                                                                                                                                                                            IDENTITY_NUC Gapop 10.0 , Gapop 10.0
                                                                                                                                                                                          US-09-939-853A-140
20
                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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18994
18994
34063
                                                                                      - nucleic search,
                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                        Title:
Perfect score:
                                                                                      OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                       Run on:
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Gaps

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us-09-939-853a-140.rni

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RESULT 6
US-09-620-312D-925
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                                                                                                                                                                                                                                                                                  Sequence 431, Application US/09071035
Sequence 431, Application US/09071035
Sequence 431, Application US/09071035
SENERAL INFORMATION:
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRIE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 429, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
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                                                                     DB 4; Length 303;
                                                                                                               3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIF: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
76.0%; Score 15.2; D.
Best Local Similarity 85.0%; Pred, No. 89;
Matches 17; Conservative 0; Mismatches
                                                                 Query Match
76.0%; Score 15.2; D
Best Local Similarity 85.0%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cresacaderecestrire 449
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NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB369

TELEPHONE: (301) 309-8512

INFORMATION FOR SEO ID NO: 431:

SEQUENCE CHARACTERISTICS:
LENGTH: 1515 base pairs
                                                                                                                                                                                                 250 crácacacacacacacriric 231
                                                                                                                                                       1 CTGGACAGGTTAGGGCTTTG 20
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-09-071-035-429
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GENERAL INFORMATION:

Facture No. 6617156

GENERAL INFORMATION:

FAPLICATIVE LY DOUGE LESTAMM Et al

FILE OF INVENTION: WUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR FILING DATE: 1997-08-15

SEQ ID NO 3193

FRIOR LENGTH LA 2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                    STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATION SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.0%; Score 15.2; Di
Best Local Similarity 85.0%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches
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Best Local Similarity 85.0%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                               SOFTWARE ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
ATOMES: ATOMES:
REGISTRATION NUMBER: BLOOKES
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMUCNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: A29:
SEQUENCE CHARACTER SICKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  690 crácacadaracacarciria 709
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: 9410 Key West Avenue
Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1803 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-134-000C-3193
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Gaps
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                                                                                           DB 4; Length 3614;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1454, Application US/09621976
Patent No. 6639063
JGENERAL INFORMATION:
APPLICANT: Unas Milne Edwards, J.B.
APPLICANT: Glochano, J.Y.
JAPLICANT: Glochano, J.Y.
TITLE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILION DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
IENGTH: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.0%; Score 15.2; DB 3; Best Local Similarity 85.0%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08920422A

Batent No. 625473
GENERAL INFORMATION:
APPLICANT: Witch, Michael P.
APPLICANT: Michael P.
APPLICANT: Michael P.
TITLE OF INVENTION:
FILE REFERENCE: VITEKPESSENILIN
CURRENT APPLICATION NUMBER: US/08/920,422A
CURRENT FILING DATE: 1997-08-29
NUMBER OF ESQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                        Query Match
76.0%; Score 15.2; D
Best Local Similarity 85.0%; Pred. No. 1e+0
Matches 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                       1600 caggacarrrragggcrrrg 1581
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1 LOCATION: 254

2 CTHER INFORMATION: n=a, g, c or t

US-09-621-976-14354
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  ; NAME/KEY: CDS
; LOCATION: (217)...(3411)
US-09-221-013A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Mus musculus US-08-920-422-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-621-976-14354/c
                                                                                                                                                                                                                                                                                                           US-08-920-422-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 48974
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APPLICANT: Arioli, Antonio
APPLICANT: Williamson, Richard E.
APPLICANT: Williamson, Richard E.
APPLICANT: Williamson, Richard E.
APPLICANT: Peng, Liangcai S.
APPLICANT: Peng, Liangcai S.
TILB OF INVENTION: Manipulation of cellulose and/or Beta-1,4-glucan FILE REFERENCE: 96-98
CURRENT PILING DATE: 1998-12-23
CURRENT APPLICATION NUMBER: PCT/AU97/00402
PRIOR APPLICATION NUMBER: AU PO0699
PRIOR PLING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 9
LENGTH: 3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILE REFERENCE: 784CTP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25,317
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt. Ft. genes Version 1.0
SOFTWARE: pt. Ft. genes Version 1.0
LENGTH: 2611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.0%; Score 15.2; D Best Local Similarity 85.0%; Pred. No. 98; Matches 17; Conservative 0; Mismatches
Sequence 925, Application US/09620312D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09221013A
Patent No. 6495740
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ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                     Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                     en, Feiyan
nen, Rui-hong
                                                               APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
                                                                                                                                                                                               Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (290)..(1885)
US-09-620-312D-925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .09-221-013A-9/C
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US-08-467-574-1/c
                                                                                            CITY: LOS
STATE: CA
COUNTRY:
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Sequence 1, Application US/08466589
; Sequence 1, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
APPLICANT: Ellist, Kathryn J.
APPLICANT: Ellist, Steven B.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: HECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
CORRESPONDENCE ADDRESS:
ADDRESSE: Brown, Martin, Haller & McClaim
STREET: 1660 Union Street
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-700-656-1/c
| Sequence 1, Application US/08700636
| Sequence 1, Application US/08700636
| Patent No. 5910582
| GENERAL INFORMATION:
| APPLICANT: Blist, Steven B.
| APPLICANT: Blist, Steven B.
| APPLICANT: Harpold, Michael M.
| TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME; NUMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%; Score 14.8; DB 2; Length 2068; 88.9%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 92101-2926
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OOFERATURG SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION: 3.36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: MATCH 8, 1993
ATTONNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 dercadercadederrid 127
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SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.9
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: CDS
; LOCATION: 166..1752
US-08-466-589-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
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APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBERS OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClaim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                      COMPUTER READABLE FORM;

COMPUTER READABLE FORM;

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CORPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTION DATA:

APPLICATION NUMBER: US/08/700,636

FILING DATE: 16-JUL-1996

CLASSIFICATION NUMBER: US/08/028,031

FILING DATE: 00-MAR-1993

ATTONARY/AGENT INPORMATION:

NAME: RELIEFA: 01-96-96-9392

REGISTRATION NUMBER: 31,192

REGISTRATION NUMBER: 31,192

REGISTRATION NUMBER: 31,192

REGISTRATION NUMBER: 31,192

REGISTRATION NUMBER: 31,192

RELEPAN: 619-546-4737

TELEPHONE: 619-546-4737

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TELEPHONE: 619-546-4737

TELEPHONE: 619-546-4737

TELEPHONE: 619-546-4737

TYPE: MINICHARACTERISTICS:

LENGTH: 2068 base pairs

TYPE: MINICHARACTERISTICS:

LENGTH: 2068 base pairs

TYPE: MINICHARACTERISTICS:

LENGTH: 2068 base pairs
          Brueggemann & Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.0%; Score 14.8; DB 2; Best Local Similarity 88.9%; Pred. No. 1.5e+02; Matches 16; Conservative 0; Mismatches 2;
SEE: Pretty, Schroeder, Brueggemann & Pretty, South Flower Street, Suite 2000 Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREEF: Brown, Martin, Haller & McClaim STREEF: 1660 Union Street STATE: CA STATE: CA COUNTRY: USA ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08467574 Patent No. 6022704 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGACAGGTTAGGGCTTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
NEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 166.1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COR
OPERATING SYSTEM:
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APPLICANT: Elliot, Kathryn J. Ellis, Steven B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09892985
Patent No. 6664375
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 GGTCAGGTCAGGGCTTTG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGACAGGTTAGGGCTTTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92037
COMPUTER READABLE FORM:
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STRANDEDNESS: both
                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2068 base pairs
          TELEFAX: 619-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: both
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                            NAME/KEY: CDS
; LOCATION: 166..1752
US-09-217-345-1
                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                        TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-892-985-1/c
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Patent No. 6303753

Patent No. 6303753

Patent No. 6303763

APPLICANT: Elliot, Kathryn J.

APPLICANT: Elliot, Steven B.

APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEB: Heller Ehrman White & McAuliffe

STREET: 4250 Executive Square, 7th Floor

CITY: La Jolla

STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DB 3; Length 2068; Pred. No. 1.5e+02; 0; Mismatches 2; Indels 0
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE: March 8, 1993
ATTORNEY/AGENT INPORMATION:
NAME: Seidaman, Stephanie L
REGISTRATION NUMBER: 33, 779
REFERENCE/DOCKET NUMBER: 6362-9949
TELECHONICATION INPORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0999
TELEFAX: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGRATION CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
STRANDENESS: DOTH
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDISKette
COMPUTER: DISKette
COMPUTER: DISKETCE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-UNN-95
FILING DATE: 05-UNN-95
FILING DATE: 05-UNN-95
FILING DATE: 05-UNN-95
FILING DATE: 05-UNN-95
FILING DATE: 06-WAR-93
APPLICATION UNDRER: US 08/028,031
FILING DATE: 08-WAR-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 GGTCAGGTCAGGGCTTTG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 166..1752
US-08-467-574-1
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92037
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US-09-217-345-1/c
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Harpold, Michael M.
TILLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
                                                            Gaps
                                                         ö
Query Match 74.0%; Score 14.8; DB 4; Length 2068; Best Local Similarity 88.9%; Pred. No. 1.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, 7th Floor CITY: ia Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER KEADALBLE FORKA:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

COMPERATION SYSTEM: DOS

SOFTWARE: FastESD, Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 09/82,985

FILING DATE: 27-Jun-2001

PRIOR APPLICATION NUMBER: US 09/217,345

APPLICATION NUMBER: US 08/467,574

FILING DATE: 02-JUN-95

APPLICATION NUMBER: US 08/466,589,

FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/028,031

ATTORNEY/AGENT INFORMATION:

NAWE: Seldman, Stephanie L

REGISTRATION NUMBER: 23,779

REFERENCE/DOCKET NUMBER: 24735-9949B

TELECOMMUNICATION NUMBER: 23,779
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                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ellis, Steven J.
APPLICANT: Ellis, Steven M.
APPLICANT: Ellis, Steven M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES:
Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                  Score 14.8; DB 4; Length 2068; Pred. No. 1.5e+02; 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAL.
STATE: CA
STATE: CA
COUNTRY: U.S.A.
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,855A
FILING DATE: 20-JUN-1995
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-NOV-1993
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Scientan, Stephanie
REFERENC/DOCKET NUMBER: 6362-9369B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0099
TELEPHONE: 619-238-0062
SEQUENCE CHARACTER/STICS:
LENGTH: 2277 Dase pairs
TYPE: nucleic acid
"ANDEDNESS: Doch
TYPE: ODCH
                                       LOCATION: 166..1752
SEQUENCE DESCRIPTION: SEQ ID NO: 1;
                                                                                                                                                                                                                                                                                                                               US-08-496-855A-1/c
; Sequence 1, Application US/08496855A
; Patent No. 5801232
                                                                                                                                                                                                           3 GGACAGGITAGGGCTTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GGACAGGTTAGGGCTTTG 20
                                                                                                                    Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: CDS
; LOCATION: 166..1755
US-08-496-855A-1
FEATURE:
                                                                               US-09-892-985-1
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Search completed: February 20, 2004, 01:45:09 Job time : 6.2454 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

February 19, 2004, 23:23:34; Search time 48.0735 Seconds (without alignments) 1456.787 Million cell updates/sec Run on:

US-09-939-853A-140 20

1 ctggacaggttagggctttg 20 Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2308684 segs, 1750822206 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:\*

1: /cgu2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
2: /cgr2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
3: /cgr2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
4: /cgr2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
5: /cgr2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
6: /cgr2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
7: /cgr2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
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9: /cgr2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
10: /cgr2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
11: /cgr2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
12: /cgr2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
13: /cgr2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
14: /cgr2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
15: /cgr2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
16: /cgr2\_6/ptodata/2/pubpna/US00\_PUBCOMB.seq:\*
17: /cgr2\_6/ptodata/2/pubpna/US00\_PUBCOMB.seq:\*
18: /cgr2\_6/ptodata/2/pubpna/US00\_PUBCOMB.seq:\*
19: /cgr2\_6/ptodata/2/pubpna/US00\_NEW\_PUB.seq:\*
11: /cgr2\_6/ptodata/2/pubpna/US00\_NEW\_PUB.seq:\*
11: /cgr2\_6/ptodata/2/pubpna/US00\_NEW\_PUB.seq:\*
11: /cgr2\_6/ptodata/2/pubpna/US00\_NEW\_PUB.seq:\*
11: /cgr2\_6/ptodata/2/pubpna/US00\_NEW\_PUB.seq:\*
11: /cgr2\_6/ptodata/2/pubpna/US00\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 951, App	Sequence 953, App	Sequence 21302, A	Sequence 25371, A	Sequence 133814,	Sequence 795, App			_	Sequence 35904, A	Sequence 27228, A	Sequence 137211,	Sequence 208024,	Sequence 295, App	Sequence 121358,
ΩI	US-09-867-550-951	US-09-867-550-953	US-09-814-353-21302	US-10-242-535A-25371	US-10-027-632-133814	US-10-094-749-795	US-10-027-632-103042	US-10-027-632-103043	US-10-108-260A-602	US-09-918-995-35904	US-09-918-995-27228	US-10-027-632-137211	US-10-027-632-208024	US-09-882-227-295	US-10-424-599-121358
DB	6	σ	10	15	15	15	15	15	15	10	10	15		10	12
Suery Match Length DB	444	763	864	422	665	2305	2424	2424	3559	403	467	570	663	1152	1744
Query Match	100.0	100.0	100.0	87.0	84.0	84.0	84.0	84.0	84.0	79.0	79.0	79.0	79.0	79.0	79.0
Score	20	20	20	17.4	16.8	16.8	16.8	16.8	16.8	15.8	15.8	15.8	15.8	15.8	15.8
Result No.	0	0	n O	4	ιΩ	y U	0	<b>6</b> 0	о О	10	11	12	13	14	15

Sequence 73670, A		23,		1, 1	Sequence 3, Appli	Sequence 1299, Ap	Sequence 144930,		Sequence 169996,		Seguence 121172,	405	Sequence 610, App	301	244		Sequence 7, Appli		80	Sequence 408, App	Sequence 408, App	34,		202	Sequence 1752, Ap	Sequence 32274, A			Sequence 303041,
US-10-424-599-73670					US-09-816-095-3	US-09-917-800A-1299	US-10-027-632-144930	US-10-027-632-169995	US-10-027-632-169996	US-10-027-632-121171	US-10-027-632-121172	US-10-101-510-405	US-10-225-567A-610	US-09-930-213-301	US-10-085-117-244	US-09-836-607-7	US-09-421-112-7	US-10-106-698-3422	US-09-764-869-408	US-10-091-504-408	US-10-227-577-408	US-09-836-607-34	US-09-421-112-34		US-09-918-99	US-09-918-995-32274	US-10-027-632-36047	US-10-027-632-61127	US-10-027-632-303041
12	10	14	15	13	σ	თ	12	15	15	12	12	14	14	2	15	σ	5	14	Q	14	15	σ	10	10	10	10	15	15	15
1824	4170	4170	4359	24023	99916	673	761	786	786	978	978	2067	3685	4112	136726	309	309	320	430	430	430	468	468	472	475	478	547	547	547
79.0	79.0	79.0	79.0	79.0	79.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0
15.8	15.8	15.8	15.8	15.8	15.8	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2
16	17	18	19	20	21	22	23	24	25	c. 26	c 27	28	29	c 30	31	c 35	33	C 34	c 35	c 36	c 37	38	39	α 40	c 41	c 42	43	C 44	c 45

## ALIGNMENTS

```
Sequence 951, Application US/09867550
Patent No. US20020082206A1
Patent No. US20020082206A1
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Law, Debbis APPLICANT: Law, Debbis APPLICANT: Law, Debbis APPLICANT: Topper, James
APPLICANT: Topper, James
TITLE OF INVENTION: N. US20020082206A1e1 Polymucleotides from Atherogenic Cells and F TITLE OF INVENTION: Thereby
TITLE DE INVENTION: Thereby
TITLE DE INVENTION: Thereby
TITLE APPLICATION NUMBER: USSN 60/208,427
FRICK APPLICATION NUMBER: USSN 60/208,427
FRICK APPLICATION NUMBER: USSN 60/208,427
FRICK APPLICATION NUMBER: USSN 60/208,427
FRICK ELING DATE: 2000-05-30
NUMBER OF SEC ID NOS: 2125
CONTING DATE: PASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
US-09-867-550-951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 951
LENGTH: 444
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Query Match 100.0%; Score 20; DB 9; Length 444; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 20; Conservative 0; Mismatches 0; Indels ઠે

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Gaps ö

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RESULT 2 US-09-867-550-953/c

; Sequence 953, Application US/09867550 ; Patent No. US20020082206A1

```
APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005

CURRENT APPLICATION UNMER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085,783

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

NUMBER OF SEQ ID NOS: 58994
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APPLICANT: WIS CONTROLLING:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US,10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 1000-03-24
PRIOR PILING DATE: 1000-03-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 87.0%; Score 17.4; DB 15;
Best Local Similarity 94.7%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                     Sequence 25371, Application US/10242535A Publication No. US20040013663A1 GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 133814, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
| LOCATION: (406) ... (406)
| OTHER INFORMATION: n is a; c, g, or t
US-10-242-5354-25371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or
t
                                                                                                                                      353 crddacaderraeddcrrre 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 crecacacerracecrrr 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (7)._(7)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (5). (5)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (5)..(5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-027-632-133814
                                                                                                                                                                                                                                                        US-10-242-535A-25371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 25371
                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
APPLICANT: Mehraban, Fuad,
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2401-09-20
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
FRIOR APPLICATION NUMBER: US/08/427
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 953
LENGTH: 763
TYPE: NN'
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APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Illie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: ITERAPY OF OVARIAN CANCER
FILE REPERENCE: MAI-0068
CURRENT FILING DATE: 2001-03-21
FRIOR APPLICATION NUMBER: US 60/29/814,353
CURRENT FILING DATE: 2000-05-25
FRIOR APPLICATION NUMBER: US 60/207,124
FRIOR APPLICATION NUMBER: US 60/211,940
FRIOR FILING DATE: 2000-06-15
FRIOR APPLICATION NUMBER: US 60/216,820
FRIOR APPLICATION NUMBER: US 60/220,661
FRIOR APPLICATION NUMBER: US 60/220,661
FRIOR APPLICATION NUMBER: US 60/220,661
FRIOR APPLICATION NUMBER: US 60/220,661
FRIOR APPLICATION NUMBER: US 60/220,661
FRIOR FILING DATE: 2000-07-25
FRIOR APPLICATION NUMBER: US 60/220,661
FRIOR FILING DATE: 2000-07-25
FRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE FRANCE RESERVED
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Best Local Similarity 100.0%; Score 20; DB 10; Length 864;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels C
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Publication No. US20030165831A1
GENERAL INFORMATION:
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; LOCATION: 1, 2, 3, 32, 862, 863, 864

; CTHER INFORMATION: n = A,T,C or G

US-09-814-353-21302
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Matches 20; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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CRGANISM: Homo sapiens
US-09-867-550-953
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LENGTH: 864
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1 CTGGACAGGTTAGGGCTTTG 20

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TYPE: DNA

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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PAPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PELING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1994-09-28
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Pred. No. 53;
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Pred. No. 53;
0; Mismatches 2;
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90.0%;
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-10-027-632-103043
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Pred. No. 53;
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APPLICANT: SEXI, NACHIKO
APPLICANT: SEXI, NACHIKO
APPLICANT: SEXI, NACHIKO
APPLICANT: STUTCAN
APPLICANT: YOSHIKAWA, TSUTCMU
APPLICANT: YOSHIKAWA, TSUTCMU
APPLICANT: NACHHRI, KENI
APPLICANT: NACHHRI, KENI
APPLICANT: MASUHO, YASUHIKO
TITLE NET ERRERNCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
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                                            PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 133814
LENGTH: 665
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-027-632-103042/c
; Sequence 103042, Application US/10027632
; Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 795, Application US/10094749
Publication No. US20030219741A1
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APPLICANT: 5UGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TESSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUKI
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Best Local Similarity 90.0%;
Matches 18; Conservative (
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OTSUKA, KAORU
NAGAI, KEIICHI
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                                                                                                                                                                                                                                  ; ORGANISM: Human
US-10-027-632-133814
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Matches

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FIREAL INCRMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 2000-03-24

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PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-09-18

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PRIOR PE
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                                        INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.0%; Score 15.8; DB 15;
89.5%; Pred. No. 1.7e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.0%; Score 15.8; DB 10; Best Local Similarity 89.5%; Pred. No. 1.7e+02; Matches 17; Conservative 0; Mismatches 2;
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUER
TITLE OF INVENTION: ROOM VARIOUS CDNA LIBRAA;
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRAA;
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILLIG DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILIOR DATE: 1999-01-20
PRIOR PILIOR DATE: 1999-01-20
SEQ ID NO 2228
SEQ ID NO 2228
LENGTH: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 137211, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(467)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27228
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-027-632-208024
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LENGTH: 570
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Publication No. US2030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20011-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PLILUNG DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 30054
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FREESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                   MSS-10-108-260A-602/c

Sequence 602, Application US/10108260A

Publication No. US20040005560A1

GENERAL INTORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-AD10
CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 602
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Best Local Similarity 90.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches
          0; Mismatches
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                                                                                                                                              1453 CTGGACAGTTTAGGGCTGTG 1434

', LOCATION: (1)...(403)
', OTHER INFORMATION: n = A,T,C or G
US-09-918-995-35904

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          Conservative
                                                                            1 CTGGACAGGTTAGGG
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-10-108-260A-602
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US-09-918-995-27228
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LENGTH: 403
          18;
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Sequence 121388, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEG ID NOS: 285684
SEQ ID NO 121358
LENGTH: 1744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_80594C.1 US-10-424-599-121358
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                                                                       934 CTAGACGGGTTAGGGCTTT 952
                            1 CIGGACAGGITAGGGCTIT 19
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Sequence 295, Application US/0982227

Sequence 295, Application US/0982227

Sequence 295, Application US/0982227

Sequence 295, Application No. US2030158396A1

SENDICANT: No-Coment Al-Garawi, Amal

APPLICANT: Al-Garawi, Amal

APPLICANT: Al-Garawi, Amal

APPLICANT: Tomb, Jean-Francois

APPLICANT: Tomb, Jean-Francois

APPLICANT: Miller, Charles

APPLICANT: Miller, Charles

APPLICANT: Miller, Charles

APPLICANT: Miller, Coment, Raymond P.

TITLE OF INVENTION: Encoding No. US20030158396A1e1 Helicobacter Polypeptides in the

TITLE OF INVENTION: Genome

TITLE OF INVENTION Genome

TITLE OF INVENTION NUMBER: US/09/882,227

CURRENT APPLICATION NUMBER: US/09/882,227

CURRENT APPLICATION NUMBER: US 08/902,615

PRIOR FILING DATE: 1997-07-29

NUMBER OF SEQ ID NOS: 638

SOFTWARE: PSESEQ for Windows Version 4.0

SEQ ID NO 295

LEMETH: 1152
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Sequence 208024, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/198,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 1999-01-32

PRIOR PLING DATE: 1999-01-32

PRIOR PLING DATE: 1999-09-38

PRIOR FILING DATE: 1999-09-38

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FRANCE OF WINDOWS VEFSION 4.0

SEQ ID NO 208024

LENGTH 663

LENGTH 663
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Pred. No. 1.78+02;
0; Mismatches 2; Indels 0;
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Pred. No. 1.7e+02;
0; Mismatches 2;
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Best Local Similarity 89.5%;
Matches 17; Conservative (
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Best Local Similarity
Matches 17; Conserv
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US-10-027-632-208024
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; LOCATION: (52)
US-09-882-227-295
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February 19, 2004, 21:21:18 ; Search time 113.831 Seconds (without alignments) 9899.970 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                      3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_htg_mus: *
em_htg_pln: *
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DB seq length: 200000000
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Gaps

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100.0%; Score 26; DB 6; Length 1183; ilarity 100.0%; Pred. No. 0.37; Conservative 0; Mismatches 0; Indels (
       /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                              1 CCTTCTGGAAGTCTGCCAGTGTCCTT 26
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BC042041.1 GI:27469842
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Homo sapiens
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BC042041/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proteins and nucleic acids encoding same
Patent: WO 0216599-A 74 28-FEB-2002;
Curagen Corporation (US); COR THERAPEUTICS, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burgess, C.E., Conley, P.B., Grosse, W.M., Hart, M., Kekuda, R., Shimkets, R.A., Spytek, K.A., Szekeres, E.S., Tomlinson, J.E., Proper, J.N. and Yang, R.B.
Proteins and nucleic acids encoding same
Patent: WO 0216599-A 76 28-FEB-2002;
Curagen Corporation (US) ; COR THERAPEUTICS, INC. (US)
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Patent: WO 0216599-A 141 28-FEB-2002;
Curagen Corporation (US) ; COR THERAPEUTICS, INC. (US)
Location/Qualifiers
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                                                                    /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                      /note="oligonucleotide primer"
                                                                                                                                                                      100.0%; Score 26; DB 6;
llarity 100.0%; Pred. No. 0.56;
Conservative 0; Mismatches
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/db_xref="taxon:9606"
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Sequence 74 from Patent WO0216599.
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Sequence 76 from Patent WO0216599
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Manmataria butneria; Filmaces; Cacaiiniii; Howiniidae; Howe.

Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausherr, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.W., Sodergren, B.J., Lu, X., Glubbs, R.A.,
Butlerialon, C., Rating, M., Madan, A., Young, A.C., Shevchenko, Y.
Boutfazd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalius, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-femail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center; Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                               PRI 07-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 88 Row: a Column: 20
                                                                                                                                                                                                                          BC042041

Homo sapiens Src-like-adaptor 2, transcript variant 1, mRNA (cDNA clone MGC:49845 IMAGE:4429896), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Direct Submission
Submitted (23-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. Ū.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
908 cchrchedaachcheccachchchr 933
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Gaps

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PAT 14-JUL-2003

FEATURES

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Human DNA sequence from clone RP3-460J8 on chromosome 20q11.21-11.23 Contains the 3' end of the gene for a novel protein similar to N-myc downstream regulated (NDRG1) the 5' end of a gene encoding a novel protein tyrosine kinase, ESTs, STSs and GSSs, AL031662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (23-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (23-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
Control of the Sequence action replaced gi:6425549.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 66741)

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                                                                                 6; Length 2567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Score 26; DB 6; Length 2788;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 26; Conservative 0; Mismatches 0; Indels (
                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                              DNA
                                                                            Score 26; DB 6
Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                    AX780857 2788 bp DNJ
Sequence 3014 from Patent WO03039443.
AX780857
                                                                                                                       0; Mismatches
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/mol_type="unassigned DNA"
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HTG; NDRG1; SH2 domain.
Homo sapiens (human)
Homo sapiens
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1 Similarity 100.0%;
26; Conservative 0
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DEFINITION
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AX780857/c
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KAEBLLLLGRONDGGAFLIREGGTRRGSYSLSVRLASRPAKWBERRHYRTHGLDMGWLYI
SPRLTPPSLGALWPYSELADDICCLLKEPOVLQRAPPPGKDIPLPYVUQRTPLNWK
ELDSSLLFSEAATGEESLLSEGLRESLSFYISLNDEAVSLDDA"
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28416422. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation="MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SH3; Region: SH3 domain. SH3 (Src homology 3) domains are often indicative of a protein involved in signal transduction related to cytoskeletal organization. First described in the Src oytoplasmic tyrosine kinase. The structure is a partly opened beta barrel" // Ab xref="CDD:pfam00018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang, H., Yang, W.P., Wu, Y., Whitney, G.S., relestities, S. S. Kanner, S.B. Cloning and expression of human slap-2: a novel sh2/sh3 domain-containing human slap homologue having immune cell-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                      /organism="Homo sapiens"
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/lab host="DH108"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Src-like-adaptor 2, isoform
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db_xref="GI:27469843"
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/db_xref="CDD:pfam00017"
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Bristol-Myers Squibb Co. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            db_xref="LocusID:84174"
db_xref="MIM:606577"
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1 Similarity 100.0%; Pred. No. '
26; Conservative 0; Mismatch
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Sequence 1 from Patent W00242457.
AX452880 GI:21712520
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gene="SLA2"
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AX452880/c
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polyA_site
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMED. Sw., SMISSPROT, Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at which sanger ac.uk/Polets/Celegans/wormpep This sequence chromosome 20 was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 happing Group. Further information can be found at hittp://www.sanger.ac.uk/HGP/Chr20

INFORTANT: This sequence is not the entire insert of clone RP3-4604B If may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP3-4604B is at 66741 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1:e., phred quality = 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone, and the assembly was confirmed by the group of Pieter de Jong. For http://www.chori.org/bacpac/home.htm

VECTOR: PCTOR: PCTOR: PCTOR.
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| db_xref== SWISS-PROT:Q9H6Q3"
| translation="MGSLPSRRKSLPSPSLSSSVQGQGPVTMBAERSKATAVALGSFP
AGGPAELSIRLGEPFTIVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/db_xref="d1:15020830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(<240. .339,6995. .7128))
/gene="dJ977B1.1"
/product="dJ460J8.2 (novel protein tyrosine kinase with
/product="dJ460J8.2 (sp.) domain )"
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match: ESTs: Em:BG178487"
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note="15 copies 2 mer ag 93% conserved"
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/clone lib="RPC1-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Em:T989705 Em:AT786673 Em:A1181197 Em:AA7464653 Em:AA316771
Em:AU035165 Em:AV002368"
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HPGOBELOĀNLDLIGYTSKHIAQDINQDNLOĻFLMSYNGRENLEIBRPILGQNNKS

KTLKCSTLLVVGDNSPAVBAVVECNSRLNPINTTLLKWADCGGLPQVVQPGKLTBAFK

YFLQGMGYIPYQQDSPASANTRLARSRTHSTSSSLGSGESPFSRSVTSNQS

DGTDESCESPDVLDRHQTMRVSC"

COMDIEMENT (24246. . 24780)
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NFSDWQBITQHFAVCHVDAPGQGGGAPSFFTGYQYPTMDBLABMLPPVLTHLSLKSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 match: proteins: Sw:Q62433 Sw:Q92597 Tr:Q9Z2L9 Sw:P97862"
                                                                                                                                                                                                                                                                                                                                                                                                                 complement (17523. . 54534)
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/note="HYX repeat: matches 1. .109 of consensus"
34505. .34560
/note="28 copies 2 mer ta 78% conserved"
34564. .34611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="novel protein (FLJ13556) similar to N-myc downstream regulated (NDRG1)
                                                                                                                                                                                    note="MER21B repeat: matches 355. .374 of 4746. .15078
13 copies 2 mer tt 92% conserved"
.13961
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                                                                                                                                                                                                                                                                                                                                                               note="match: GSS: Em:AZ067993"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein id="CAB65625.1"
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                                                                                                                                                                                                                                                                                                                                                                                          complement (17521)
complement (17522)
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contig of
gap of 100
contig of
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17149
17249
19240
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31620
31720
34680
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                                                                                                              TITLE
JOURNAL
                                                                                                                                                                              COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC026539 145833 bp DNA linear HTG 27-APR-2000 Homo sapiens chromosome 20 clone RP11-712N14 map 20, WORKING DRAFT SEQUENCE, 37 unordered pieces.
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hote="TIGGER2 repeat: matches 1780. .2541 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="TIGGER2 repeat: matches 2541. .2714 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                             note="MER52C repeat: matches 1. .1278 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60719. .61831
70tt="MER11C repeat: matches 1. .1071 of consensus"
62847. .63174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
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Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="73 copies 2 mer at 83% conserved"
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59062. .59236
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49391. 49480

/note="45 copies 2 mer ta 76% conserved"

52922. 53120

hote="match: STS: Em:G04621"

/gene="dJ469A13.3"
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Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens chromosome 20, clone RP11-712N14
                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ310681"
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                                                                                                                                                                                                                                /note="match: GSS: Em:AQ314824
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54054. .54477
                                                                                                                                                                                                                                                                                                                                            /note="match: STS: Em:G07504"
complement(57696. .58013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Score 26; DB
Best Local Similarity 100.0%; Pred, No. 0.2
Matches 26; Conservative 0; Mismatches
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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AC026539/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Matches
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Voh., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Direct Submission.

L. Submitted (12 MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Apr 27, 2000 this sequence version replaced gi:7283243.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project Information
Center project name: L/115
Center clone name: 712_N.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4: contig of 1214 bp in length

4: gap of 100 bp

5: contig of 1359 bp in length

5: contig of 13747 bp in length

6: contig of 1341 bp in length

7: contig of 1341 bp in length

7: contig of 1888 bp in length

8: contig of 1888 bp in length

8: contig of 1898 bp in length

8: contig of 1898 bp in length

8: gap of 100 bp

8: contig of 1835 bp in length

8: contig of 1835 bp in length

8: contig of 1835 bp in length

8: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00 bp
f 2848 bp in length
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2666 bp in length
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f 1763 bp in length
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2169 bp in length
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of 2311 bp in length
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contig of 2848 bp ...
gap of 100 bp
contig of 2666 bp in
gap of 100 bp
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) bp 2960 bp in length

100 bp of 2748 bp in length

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100 bp of 5872 pm length 100 bp of 8826 bp in length 100 bp 100 bp
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                                                                                                100 bp
of 3290 bp in length
                                                                                                                                                                                                                                                                                               100 bp
of 4775 bp in length
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of 5730 bp in length
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of 3790 bp in length
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of 5701 bp in length
                                                100 bp
of 3497 bp in length
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Algarie., C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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On Oct 11, 2002 this sequence version replaced gi:21988900.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist enricely of whole genome shotgun sequence reads Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
Mawhiney, S., McLead, M. P., Martli, K., Menen, E., Martlinez, E., Mandray, McNeall, T. Z., Menen, E., Mores, S., Miloavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Miloavljevic, A., Morris, S., Mundasa, M., Murphy, M., Nari, L., Nankervis, C., Neal, D., Newton, M., Murphy, M., Naris, S., Nandelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Padl, H., Perez, J., Perez, L., Pelankoch, C., Plopper, P., Poinderer, A., Perez, L., Pelankoch, C., Pointak, S., Padl, H., Perez, J., Peter, E., Pul, L., Plazor, M., Rachlin, R., Rachlin, E., Reves, R., Redier, M., Reigh, R., Reilly, B., Railly, M., Ren, Y., Reuter, M., Richards, S., Rigs, F., Sanders, W., Savery, G., Scherer, S., Scott, G., Shataman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D. Smajs, D., Sheetty, J., Shvartsbeyn, A., Sisson, I., Stater, C.D. Smajs, D., Sheetty, J., Shvartsbeyn, A., Sisson, I., Stater, C.D. Smajs, D., Sheetty, J., Shvartsbeyn, A., Sisson, I., Stater, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Trapey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wight, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, U., Yakub, S., Yen, J., Yoon, L., Yoon, V., Weinster, A., Shate, S., Smith, H.O., Neiss, R., Smith, D.R., Smith, H.O., Neiss, R., Smith, D.R., Smith, R., Smith, R., Smith, R., Smith, S., Smith, R., Smith, S., Smith, R., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smith, S., Smit
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (27-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Genter clone name: CH310-251F22

Assembly program: Phrap; version 0.990329
Consenus quality: 155282 bases at least Q40
Consensus quality: 159515 bases at least Q20
Consensus quality: 159515 bases at least Q20
Estimated insert size: 155592; sum-of-contigs estimation
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Rat Genome Sequencing Consortium.
Direct Submission
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JOURNAL
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

AUTHORS REFERENCE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17949;)

2 1 (bases 1 to 17949;)

3 Alsbrooks, S.L., Amaratunge, H.C., Are J.R., Ayele, M., Banks, T., Barboria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Burbar, C., Burch, P., Brewa, M., Brown, R., Brown, M., Bryant, N.P., Burbar, C., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chakis, Chavez, D., Chen, R., Chen, R., Chen, R., Chen, T., Christopoulos, C., Carter, M., Davila, M.L., Davis, C., Davy-Carroll, L., Dathorne, S.R., David, R., Delaney, K.R., Delaney, K.R., Delaney, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Dragan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Escotto, M., Falls, T., Ferraguto, D., Flangs, N., Garrer, P., Frantz, P., Falls, T., Ferraguto, D., Flags, N., Garrer, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
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Homo sapiens 3 BAC RP11-251C9 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
AC020636
AC020636.14 GI:22003934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 81.5%; Score 21.2; DB 2; Length 177004; Best Local Similarity 88.5%; Pred. No. 35; Matches 23; Conservative 0; Mismatches 3; Indels 0;
                                                                                     1 173251: contig of 173251 bp in length. 1252 173351: gap of unknown length 13352 174391: contig of 1040 bp in length 1352 174491: gap of unknown length 1492 175689: contig of 1198 bp in length 1590 175789: gap of unknown length 17004: contig of 1215 bp in length. 1 177004: contig of 1215 bp in length. 1.177004
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Overlapping clones are noted at the beginning and end of the

ANNOTATION OF FEATURES:

Peatures listing

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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., HavJak,P., Hawes,A., He,X., Hernandez,J., Hennandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Hubre,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Hume,J., Karly,S., Khan,U., Khag,L., Korvah,J., Loulseged,H., Lozado,K.M., Kureshi,A., Landry,N., Leal,B., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,M., Martinez,E., Massey,E., Martingle,A., Martingle,A., Martingle,A., Massey,E., Massey,E., Martingle,A., Mondabat,K., Mosc,S., Moscyan,M., Moorish,T., Morris,S., Moscy,M., Neal,D., Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Notedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,M., Nickerson,E., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Ovtedo,R., Pace,A., Payton,B., Pear,Y., Pace,A., Payton,B., Pear,Y., Pace,A., Payton,B., Payton,B., Payton,B., Payton,B., Payton,B., Payton,B., Payton,B., Payton,B., Payton,B., Payton,B., Payton,B., Path,E., Oulles,M., Ruiz,S., Savery,G., Scherer,S., Shen,H., Shocshtari,N., Shoson,I., Standey,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Stone,H., Ston
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Submitted (07-07M-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

at URL

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Once and Region of Sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consenues splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are amotated as similar.

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                source
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.

Submitted (15.9AR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 30, 2002 Like sequence version replaced gi:21954832. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

Direct Submission

Worley, K.

REFERENCE AUTHORS

JOURNAL

COMMENT

Submitted (14-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 179497)

Worley, K.C. Direct Submission

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* NOTE: Estimated insert size may differ from sequence length
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I (Dasses L. C. 25959).

Allen, C. Allen, H. Alsbrooks, S., Amin, A., Anguianc, D.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguianc, D.,

Anjanbechi, V., Aoyagi, A., Ayodi, M., Baca, E., Baden, H.,

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Davila, M.L., Davis, C., Davy-Carroil, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fraser, C.M., Gabisi, A., Ganta, R., Garner, T., Gebregeorgis, E., Geer, K., Gill, R., Gracia, A., Ganner, T., Gebregeorgis, E., Geer, K., Gill, R., Gracia, A., Ganner, T.,

Harvey, Y., Havlak, P., Hawes, A., Hendels, J., Hernandez, J.,

Hernandez, R., Hines, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIUSEUS 19-NOV-2002 SE9967 bp DNA linear HTG 19-NOV-2002 RATUR DRAFT SEQUENCE, 2 UNOXGERED DISCRES.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS PHASEI; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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/rpt_family="MADE1"
                                                                                                                                                                                                                                               complement(20197. .20270)
/rpt_family="L2"
21547. .21594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29519 CCATCTGGAAGTCTCCCAGTGTCCAT 29494
/rpt_family="AT_rich"
complement(15437. .15729)
/rpt_family="AluSc"
complement(15863. .16265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(CA)n"
29110. .29356
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21947, .22063
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complement(23769...2
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29684. .29788
                                                                                                                   i. .16711
family="MIR"
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KEYWORDS
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Culterc Summission.

Submitted (19-NOV-2002) Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23101542.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contigs scaffold'). Within each contig described in the feature contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence contigs within a contig-geaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                Jackson, J., Jacob, L., Jang, H., Johnson, B., Johnson, B., Johnson, J., Jackson, L., Jackson, L., Jackson, L., Jackson, L., Jang, E., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Khan, Z., Lu, J., Lu, K., Lu, Y., Lu, Y., Loulsegace, B., Lopez, J., Lu, X., Man, J., Manen, M., Mahnadarte, M., Mahnadarte, M., Mahnadarte, M., Mandloy, K., Marlox, K., Manguan, P., Martin, K., Martin, R., Martinz, E., Mandloy, K., Manguan, P., Martin, K., Martin, R., Martinz, E., Mandloy, K., Manguan, P., Martin, R., Martin, R., Martinz, E., Mandloy, K., Manguan, P., Martin, R., Martin, R., Martinz, E., Mandloy, M., Nair, I., Manguan, B., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, I., Narkelemeh, C., Okwucoun, G., Minja, E., Munidasa, M., Murphy, M., Nair, I., Perez, A., Popon, M., Martin, R., Martin, E., Reeves, K., Regier, M.A., Reigh, R., Rally, B., Reilly, M., Ren, Y., Reuter, L., Parankon, C., Roke, M., Ren, Y., Robe, M., Rose, R., Kuiz, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Shafaman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Tabg, X., Tabg, S., Tang, J., Yon, Y., Yor, Y., Villasan, D., Maldron, L., Walke, F., Wang, J., Wang, G., Wang, S., Warten, J., Walke, R., Wang, S., Warten, J., Walke, R., Wang, S., Warten, J., Walke, R., Wang, G., Wang, S., Warten, J., Walker, J., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhou, S., Dunn, D., von Nideratusern, A., Weise, R., Mille, F., Wang, S., Warten, J., Walker, J., Yon, W., Wang, S., Warten, J., Yoo, J., Yoo, Y., Wang, S., Warten, J., Walker, J., Yoo, J., You, Yu, F., Zhang, J., Zhou, X., Zhou, S., Punn, D., von, Wangh, J., Wang, S., Warten, J., Yoo, J., You, J., Yu, F., Zhang, J., Zhou, X., Zhoo, S., Dunn, D., von, Wang, S., Warten, J., Yoo, J., You, Y., Zhou, S., Dunn, D., Von, Wang, S., Warten, J., Yoo, J., Yoo, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zh
Johnson, R., Jolivet, A.,
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Center project name: GNJS
Center clone name: GNJS
Center clone name: CH230-117017
Center clone name: CH230-117017
Assembly program: Phrap; version 0.990329
Consensus quality: 218447 bases at least Q40
Consensus quality: 221950 bases at least Q30
Consensus quality: 222950 bases at least Q30
Consensus quality: 222950 bases at least Q30
Estimated insert size: 224159; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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Worley, K.C.
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AUTHORS
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS_PHASE1, HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21.2; D. Pred. No. 34; 0; Mismatches
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Best Local Similarity 88.5
Matches 23; Conservative
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AC095338/c
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AUTHORS
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ORIGIN

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Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:23096505.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Naakeris, C., Neal, D., Newcon, N., Nayen, N., Norris, S., Nwackelemeh, C., Newtonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Paperer, E., Pal, S., Parks, K., Pologer, F., Poloder, C., Primus, E., Pul, L.-L., Plopper, F., Poloder, A., Popovic, D., Primus, E., Pul, L.-L., Puzzo, M., Quiroz, J., Rachin, E., Reeves, K., Redier, M., Reilly, B., Reilly, M., Ren, Y., Reeves, K., Raiz, S., Riggs, F., Railly, B., Reilly, M., Ren, Y., Rose, M., Rose, M., Racker, M., Richards, S., Shen, H., Sanders, W., Savery, G., Scherer, S., Soct., G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steinle, M., Strong, K., Stron, A., Sacelle, M., Strong, K., Stron, W., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Valas, R., Wallson, R., Walub, S., Van, W., Willson, R., Willson, M., Wardub, S., Van, Y., Yoon, Y., Willams, G., Willson, R., Walub, S., Van, Y., Yoon, Y., Weist, R., Walub, S., Van, Y., Yoon, Y., Vu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Naser, I. L., Dupullished
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Submitted (16-SRP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 261492)
Rat Genome Sequencing Consortium.
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Consensus quality: 244697 bases at least Q40
Consensus quality: 244689 bases at least Q30
Consensus quality: 251288 bases at least Q20
Estimated insert size: 255184; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Center code: BC/M
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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Center clone name: CH230-114A11
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us-09-939-853a-141.rge

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Whitehead Institute/MIT Center for Genome
                         Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genom Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this Sequence version replaced gi:6705794.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                * NOTE: This record contains 84 individual
sequencing reads that have not been assembled into
contigg. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L4256
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Center clone name: 197_L_13
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukalalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dowino, M., Doyle, M., Fensetor, J., Ferreira, P., Firzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Landers, T., Lehocaky, J., Levine, R., Lieut, G., Liu, G., Looke, K., Macdonald, P., Marquis, M., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, W., Viel, K., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 76332)
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as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
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/db_xref="taxon:10116"
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Homo sapiens chromosome 5 clone CTB-46B19, complete sequence.
AC011405
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1 (bases 1 to 184541)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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ii gap of 100 bp contig of 825 bp in length gap of 100 bp contig of 817 bp in length gap of 100 bp contig of 802 bp in length gap of 100 bp contig of 815 bp in length gap of 100 bp contig of 806 bp in length gap of 100 bp contig of 806 bp in length gap of 100 bp contig of 806 bp in length gap of 100 bp contig of 806 bp in length gap of 100 bp contig of 806 bp in length gap of 100 bp contig of 800 bp in length gap of 100 bp contig of 800 bp in length gap of 100 bp contig of 800 bp in length gap of 100 bp contig of 800 bp in length gap of 100 bp contig of 800 bp in length gap of 100 bp contig of 800 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length
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Pred. No. 59;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7%;
Matches 22; Conservative
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60902:
61690:
61790:
62590:
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64395:
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58181:
58996:
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Homo sapiens
     Unpublished
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AC011405/c
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TITLE
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TITLE
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Gaps

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Direct Summission

Direct Summission

Cambridgeshire, CB10 189, UK. E-mail enquiries

Cambridgeshire, CB10 189, UK. E-mail enquiries

Cambridgeshire, CB10 189, UK. E-mail enquiries

Cambridgesper.ac.uk Clone requests: clonerequests.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

ya small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

one plasmid subclone or more than one MIS subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em.; EMBL; Sw.;

SWISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP

database can be found at

http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence

was generated from part of bacterial clone contrigs of human

chromosome 10, constructed by the Sanger Centre Chromosome 10

Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr10

RP11:55CS is from the library RPC11:1 constructed by the group of

pieter de Jong. For further details see

http://www.nanger.ac.uk/HGP/Chr10

RP11:55CS is from the library RPC11:1 constructed by the group of

pieter de Jong. For further details see

http://www.nanger.ac.uk/HGP/Chr10

RP11:55CS is from the library RPC1-11:1 constructed by the group of

http://www.consume.org/bacpac/home.htm

VECTOR: Paakes.6

Incentions only once except for a short everlapping

true left end of clone RP11-55CS is at 1 in this sequence.

Incenting the prop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL355474 120194 bp DNA linear PRI 09-JAN-2007
Human DNA sequence from clone RP11-55C5 on chromogome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 120194)
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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80.0%; Score 20.8; D

Best Local Similarity 91.7%; Pred. No. 54;
Matches 22; Conservative 0; Mismatches
                                  1. .184541
Acganiam.Homo sapiens"
Mol_type="genomic DNA"
Ab xref="taxon:9606"
/chromosome="S"
/clone="CTB-46819"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108454 Cricidaadricidcaachdacrr 108431
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                                         source
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AL355474/c
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
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/organism="Homo sapiens" /mol type="genomic DNA" /db xref="taxon:9606"

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DB 9; Length 120194;
                                                                               /note="Seguence from AC025038 seguenced by GTC.
                                                                                                                                                                             1; Indels
                                                                                                                                    78.5%; Score 20.4; Dilarity 95.5%; Pred. No. 87; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                 Search completed: February 19, 2004, 23:23:23
Job time : 119.831 secs
/chromosome="10"
/clone="RP11-55C5"
/clone_lib="RPCI-11.1"
39283.__39323
                                                                                                                                                                                                                                             71803 CTTCTGGAAGTCTGCCAGTGCC 71782
                                                                                                                                                                                                                 2 CTICIGGAAGICIGCCAGIGIC 23
                                                                                                                                      Query Match
Best Local Similarity
                                                           misc_feature
                                                                                                                                                                             21,
                                                                                                                                                                             Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February 19, 2004, 21:15:48; Search time 24.0879 Seconds (without alignments) 4585.415 Million cell updates/sec Run on:

US-09-939-853A-141 26 1 ccttctggaagtctgccagtgtcctt 26

Title: Perfect score:

Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

9: geneseqn2003cs:\*
10: geneseqn20 geneseqn2002s:\* geneseqn2003as:\* geneseqn2003bs:\* N Geneseq 29Jan04:\* geneseqn2001bs:\* geneseqn2001as:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

		•			SUMMALES	
Result		Query	٠			
. So.	Score	Match	Length	80	ID	Description
н	26	100.0	38	9	ABK61506	Abk61506 Human NOV
0	26	100.0	444	9	ABQ98669	Abq98669 Human ORF
m	26	100.0	445	5	AAS74747	
C 4	26	100.0	763	9	ABQ98670	Abg98670 Human ORF
υ N	26	100.0	1183	w	ABK61465	Abk61465 Human cDN
0	26	100.0	2567	φ	AAD43980	Aad43980 Human Src
7		72.3	258	œ	ACC58334	
σο		72.3	258	œ	ACC58338	Acc58338 Human abr
σ		72.3	258	æ	ACC58337	Acc58337 Mouse abr
10	18.8	72.3	258	æ	ACC58336	G
11	œ	72.3	264	9	AAD27075	Aad27075 Human uro
12	18.8	72.3		v	AAD27083	Aad27083 Human uPA
13	18.8	72.3	300	П	AAN81299	Aan81299 Human pro
14	18.8	72.3		v	AAD27078	Aad27078 Human uro
15	•	72.3	429	9	AAD27082	Aad27082 Human uPA
16	•	72.3	465	7	AAL55230	Aal55230 Tumour an
17	18.8	72.3	465	۲-	AAL55236	ø
18		72.3	482	9	ABK62674	4
19		72.3	482	σ	ADB56463	Adb56463 Toxicity-
20	18.8	72.3	482	σ	ADB50966	Adb50966 Primary r
21		72.3	618	σ	ADD35169	Add35169 Mouse mit
22		72.3	624	~	N.	Aat75153 Metastasi
23	18.8	72.3	645	N	AAT75154	Aat75154 Metastasi

700004407784500186	Aaq1019 EnCodes P Aaq10170 Encodes P Aaq23009 Pro-UK. 3 Aaq41450 Mutait hu Aaq48228 PUK gene. Aad27077 Human uro.
AAT75155 AB199589 AAT61672 AAT61673 AAC55771 AAT68737 AAT68737 AAT68737 AAT68737 AAT68737 AAT68737 AAT68737 AAT68737	AAQ10169 AAQ10170 AAQ23009 AAQ41450 AAQ48228 AAD27077
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666 689 689 1117 1128 1238 1238 1238 1238 1238 1238 1238	1236 1236 1236 1236 1236
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## ALIGNMENTS

RESULT 1

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Human; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; call signal processing disorder; metabolic pathway medulation disorder; diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; probe; uterus cancer; immune response; graft-versus-host disease; Exon linking; acquired immunodeficiancy syndrome; AlDS; asthma; Crobin's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation; AlDright hereditary osteodystrophy; reverse transcriptase PCR.
           ABK61506 standard; DNA; 26 BP.
                                                     18-JUN-2002 (first entry)
                                                                          Human NOV13 RT-PCR probe.
                                 ABK61506;
ABK61506
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WO200216599-A2. Homo sapiens.

28-FEB-2002.

27-AUG-2001; 2001WO-US026510.

25-AUG-2000; 2000US-0228191P. 08-FEB-2001; 2001US-0267300P. 20-FEB-2001; 2001US-026961P. 20-MAR-2001; 2001US-0277337P.

(CORT-) COR THERAPEUTICS INC.

Shimkets RA; Grosse WM, Hart M, Kekuda R, Shir Tomlinson JE, Topper JN, Yang R, Burgess CE, Conley PB, Spytek KA, Szekeres ES,

WPI; 2002-280937/32.

New polypeptides for treating or preventing a disorder associated with them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.

Example 2; Page 234; 263pp; English.

The invention relates to an isolated polypeptide (NOVX) a mature form of NOVX, a NOVX variant (differing by no more than 15%), the nucleotide

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encoding NOVX (or its complement, fragment or variant). NOVX is NOV1-14, 154, 155, 164, and 16b. The NOVX polypeptide, nucleic acid encoding it and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NOVX-associated disorder in humans, e.g. cardiomyopathy, atheroselevois, a disorder related to cell signal processing and antibolic pathway modulation, diabetes or cancers. The NOVX polypeptide and nucleic acids are also useful for determining the presence of predisposition to the diseases. The NOVX nucleic acid and polypeptide are specially useful in therapeutic or prophylactic applications for disorders associated with aberrant NOVX expression or activity, e.g. cancers (e.g. diencarcinoma, lymphoma, prostate cancer or uterus cancers (e.g. daenocarcinoma, lymphoma, prostate cancer or uterus immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension, congenital heart defectes, multiple sclerosis, inflammation or Albright hereditary osteodystrophy and many other diseases listed in the conditions. This is also useful in detection assays, chromosome manning the privary osteodystrophy and disease, in disease, and and also useful in detection assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping, tissue typing, diagnostic or prognostic assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present sequence is a reverse transcriptuse (RT)-PCR probe used to measure tissue specific expression of mRNA encoding a NoVX protein
       $$GGGGGGGGGGGGGGGGGGGGG
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Sequence 26 BP; 3 A; 8 C; 6 G; 9 T; 0 U; 0 Other;

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Gaps
                                           .;
0
 100.0%; Score 26; DB 6; Length 26; larity 100.0%; Pred. No. 0.064; Conservative 0; Mismatches 0; Indels
                                                                       1 CCTTCTGGAAGTCTGCCAGTGTCCTT 26
                 Local Similarity
ses 26; Conserv
Query Match
                    Best Loc
Matches
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0;

ВР Human ORF476 coding sequence ABQ98669 standard; DNA; 444 04-NOV-2002 (first entry) ABQ98669; ABQ98669/c 셤

Antinflammatory, gene therapy, human, ORFX, atherogenic, platelet, human umbilical vein endothelial cell, HUVEC, atherosclerotic plaque, cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood coagulation disorder, inflammatory disorder; ds. Cytostatic, Cardiant, Anti-allergic, Immunosuppressive, Vulnerary,

US2002082206-A1 Homo sapiens.

27-JUN-2002

30-MAY-2001; 2001US-00867550

30-MAY-2000; 2000US-0208427P. LEAC/)

LEACH M D.
MEHRABAN F.
CONLEY P B.
TOPPER J N.
LAW D. (CONL/) LAWD/) MEHR/)

Law D; Topper JN, Conley PB, Leach MD, Mehraban F,

WPI; 2002-626554/67. P-PSDB; ABP64106.

New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including

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                                                                                  The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631-ABP64681 and ABO98194-ABQ99267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilital vein endothelial cells (HUVEC) and are expressed in potential to develop atherosclerotic plaques. The ORFX polypeptides and protential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood cardiovascular disease, inflammatory disorders. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPPO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                       6; Length 444;
                                                                                                                                                                                                                                                                                                                                                Sequence 444 BP; 103 A; 128 C; 132 G; 81 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #10551.
                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 26; DB 6; 100.0%; Pred. No. 0.09;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 10551; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 CCTTCTGGAAGTCTGCCAGTGTCCTT 10
                                                Claim 2; SEQ ID NO 951; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCTTCTGGAAGTCTGCCAGTGTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS74747 standard; cDNA; 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631
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                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
1es 26; Conservative
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genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuleoride sequences have applications in polypeptide and polymuleoride sequences have applications in adjappostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and anino acid sequences. Ab564197-Ab594564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this parent did not appear in the princed specification, but was obtained in electronic format directly from WIPO at electronic format directly from WIPO at electronic format directly from WIPO at the will be princed and produces and performed and performed the constant of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet; human umbillical veiln endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder; ds.
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                                                                                                                                                                                                                                                                                                                                                               Sequence 445 BP; 89 A; 112 C; 143 G; 101 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conley PB, Topper JN, Law D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 CCTTCTGGAAGTCTGCCAGTGTCCTT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTTCTGGAAGTCTGCCAGTGTCCTT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ98670 standard; DNA; 763 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORF477 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2001; 2001US-00867550.
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Matches 26; Conserva
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CONLEY P B.
TOPPER J N.
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The present invention relates to novel human ORFX polypeptides and their

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were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HVPC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerctic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood for this pater (form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; call signal processing disorder; metabolic pathway modulation disorder; diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; immune response; graft-versus-host disease; acquired immunodeficiency syndrome; AlDS; asthma; Crohn's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation; Albright hereditary osteodystrophy.
coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated polypeptide (NOVX) a mature form of NOVX, a NOVX variant (differing by no more than 15%). the nucleotide encoding NOVX (or its complement, fragment or variant). NOVX is NOVX-14, 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic acid encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides for treating or preventing a disorder associated with them, in humans, e.g. cardiomyopathy, atherosolerosis or cancers.
                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                100.0%; Score 26; DB 6; Length 763; 100.0%; Pred. No. 0.096; 1. Indels 1. Mismatches 0; Indels
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Tomlinson JE, Topper JN, Yang R;
                                                                                                                                                                                                                                               Sequence 763 BP; 176 A; 222 C; 218 G; 147 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                1 CCTICTGGAAGICTGCCAGIGICCII 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding protein NOV13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK61465 standard; cDNA; 1183 BP.
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08-FRB-2001; 2001US-0267300P.
20-MAR-2001; 2001US-02961P.
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(CORT-) COR THERAPEUTICS INC
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                                                                                                                                                                                                                                                                                                      Local Similarity 100.
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Szekeres ES,
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and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NOVX-associated disorder in humans, e.g. cardlomyopathy, a theroscierosis, a disorder related to call signal processing and metabolic pathway modulation, diabetes or cancers. The NOVX polypeptide or predisposition to the diseases. The NOVX mucleic acid and polypeptide are specially useful in therapeutic or prophylactic applications for disorders associated with aberrant NOVX expression or activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus cancers), immune response, graft-versus-host disease, hypertension, immunodeficiency syndrome (AlDS), asthma. Crohn's disease, hypertension, hereditary osteodystrophy and many other diseases listed in the hereditation. The DNA encoding the protein is useful in gene therapy for treating the conditions. Phils is also useful in detection assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome mapping, tissue typing, diagnostic or prognostic assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present sequence encodes a NOVX protein
         $$$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 1183 BP; 251 A; 359 C; 333 G; 240 T; 0 U; 0 Other;

;; 0 100.0%; Score 26; DB 6; Length 1183; 100.0%; Pred. No. 0.1; o; Indels 0 1 CCTTCTGGAAGTCTGCCAGTGTCCTT 26 Query Match
Best Local Similarity 100.
Matches 25; Conservative ò

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276 derrerssaksierscharteit 251

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AAD43980 standard; cDNA; 2567 BP AAD43980/c 

(first entry) 13-DEC-2002 AAD43980;

Human Src-Like Adapter Protein-2 (hSLAP-2) cDNA.

Human; SH2/SH3-domain-containing adapter; Src-Like Adapter Protein-2; SLAP-2; immune disorder; signal transduction; autoimmune disease; cancer; neoplasm; inflammation disorder; rheumatoid arthritis; osteoarthritis; psoriasis; rhinitis; allergy; inflammatory bowel disease; gene therapy; Crohn's disease; systemic luque erythematosus; tissue/organ rejection; multiple sclerosis; asthma; acute respiratory distress syndrome; pulmonary disorder; dermatological; neuroprotective; gene; ss.

Homo sapiens

/\*tag= a /product= "Human SLAP-2" Socation/Qualifiers /\*tag=

WO200242457-A1

20-NOV-2001, 2001WO-US043367

30-MAY-2002

22-NOV-2000; 2000US-0252545P

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Chang H, Yang W, Wu Y, Whitney GS, Perez-Villar JJ, Kanner SB;

WPI; 2002-463632/49. P-PSDB; AAE26357.

Novel substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-Like Adapter Protein-2, useful for therapeutic

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The invention relates to a substantially purified human SH2/SH3-domain-containing adapter Polypeptide, termed Src-Like Adapter Protein-2 (SLAP-CC 2). The invention is useful for treating an immune disorder: involving the invention is useful for Streening for antagonists or inhibitors of the interaction of NSLAP-2 with cellular signalling compounds, for diagnosing, treating or preventing diseases or disorders associated with aberrant or uncontrolled completely which associate with hSLAP-2 and which provide critical signals for cell activation, and as effectors in methods to affect T-cell for cell activation, and as effectors in methods to affect T-cell continue to treat autoimmune diseases which may be caused by the preactivated T cells, in addition to other immune system related conditions, diseases, or disorders, T-cell and B-cell neoplasms, or conditions, diseases, or disorders, T-cell and B-cell neoplasms, or percentive collits, as well as to other immune system related conditions, diseases, or disorders, T-cell and B-cell neoplasms, or percentive collits, rhinitis, inflammatory bowel disease (Crohn's and ulcerative collits), allergies, particularly those involving correctivity or B-cells and T-cells, particularly those involving mast cells or eosinophils, autoimmune diseases such as systemic lupus correctivity or expirationy diseases sincluding confinement or expirationy diseases such as systemic lupus confinement or elegants syndicme, and chronic obstructive or minmonary diseases including and multiple sclerosis, particularly these provisions or minmonary diseases including and multiples sclerosis, particularly man defined the confinement or expiration or expiration and multiples sclerosis, particularly minmonary diseases including and multiples acclerosis, particularly minmonary diseases including and multiples acclerosis, particularly minmonary diseases including and multiples acclerosis, particularly minmonary diseases.
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   intervention in immunological and inflammatory disorders and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pulmonary disorder, tissue/ organ rejection and cancer. The invenuseful in gene therapy. The present sequence is human SLAP-2 cDNA
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                                                             Claim 2; Fig 1; 85pp; English.
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Best Local Similarity 100.0
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Human, abrogen, kringle, hATF-kringle, angiogenesis, inhibitor, urokinase plasminogen activator, tumour, metastasis, cytostatic, Human abrogen (hATF-kringle) coding sequence. BP ACC58334 standard; cDNA; 258 (first entry) gene therapy; gene; ss. sapiens 26-AUG-2003 ACC58334; Homo ACC58334 

partial /product= "Human abrogen" /note= "no start or stop codon" Location/Qualifiers ď /\*tag= WO2003042354-A2

22-MAY-2003.

04-SEP-2002; 2002WO-US027885.

04-SEP-2001; 2001US-0316300P

(AVET ) AVENTIS PHARM INC.

us-09-939-853a-141.rng

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The present sequence is a coding sequence for a novel human abrogen, designated hATF-kringle, comprising the human urokinase plasminogen activator kringle domain. Abrogens such as hATF-kringle are potent inhibitors of endothelial proliferation and angiogenesis. Abrogen polypeptides are capable of inhibiting or reducing cell proliferation induced by both basic fibroblast growth factor (FGF) and vascular endothelial growth factor in a specific endothelial cell proliferation assay, angiostatin only inhibits bFGR induced proliferation in this assay, vectors that expressed abrogen polypeptides in vivo were shown to reduce tumour metastasis in 2 lung cancer models. The invention provides abrogen polypeptides and polymucleotides, and methods of using these to the that an angiogenesis-related disease or disorder, e.g. tumour metastasis
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                                                                                          New abrogen polypeptide, useful for treating an angiogenesis related
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.8; DB 8; Length 258;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels 0
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/note= "no start or stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human abrogen (hATF-kringle) coding sequence.
                                                                                                                                        Claim 32; Page 24-25; 95pp; English.
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               Brockstedt D;
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                                                                                                         diseases e.g. tumor metastasis
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1 Similarity 90.9%;
20; Conservative 0
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/*tag=
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P-PSDB; ABR42617.
                                            WPI; 2003-449566/42.
               Fong TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                             P-PSDB; ABR42599
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             Nesbit M,
                                                                                                                                                                                                                                                                                                                                                               claimed)
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The present sequence is a coding sequence for a novel human abrogen, designated hATF-kringle, comprising the human urokinase plasminogen activator kringle domain. Abrogens such as hATF-kringle are potent inhibitors of endothelial proliferation and angiogenesis. Abrogen polypeptides are capable of inhibiting or reducing cell proliferation induced by both basic fibroblast growth factor (bfgp) and vascular endothelial growth factor in a specific endothelial cell proliferation assay, angiostatin only inhibits bfgF induced proliferation in this assay, wetcors that expressed abrogen polypeptides in vivo were shown to reduce tumour metastasis in 2 lung cancer models. The invention provides abrogen polypeptides and methods of using these to the an angiogenesis-related disease or disorder, e.g. tumour metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New abrogen polypeptide, useful for treating an angiogenesis related diseases e.g. tumor metastasis.
             useful for treating an angiogenesis related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; abrogen; kringle; mATF-kringle; anglogenesis; inhibitor; urokinase plasminogen activator; tumour; metastasis; cytostatic; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                               72.3%; Score 18.8; DB 8; Length 258; 90.9%; Pred. No. 1.3e+02; Live 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                   Sequence 258 BP; 61 A; 73 C; 72 G; 50 T; 0 U; 2 Other;
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/note= "no start or stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse abrogen (mATF-kringle) coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 32; Page 25-26; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                            Disclosure; Page 95; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 5 CTGGAAGTCTGCCAGTGTCCTT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACC58337 standard; cDNA; 258 BP
            New abrogen polypeptide, useful diseases e.g. tumor metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2002; 2002WO-US027885.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-449566/42.
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The present sequence is a coding sequence for a novel murine abrogen, designated hATF-kringle, comprising the mouse urokinase plasminogen activator kringle domain. Abrogens such as mATF-kringle are potent inhibitors of endothelial proliferation and angiogenesis. Abrogen polypeptides are capable of inhibiting or reducing cell proliferation induced by both basic fibroblast growth factor (FGF) and vascular endothelial growth factor in a specific endothelial control in this assay; angiostatin only inhibits bFGF induced proliferation in this assay; angiostatin only inhibits bFGF induced proliferation in this assay; accors that expressed abrogen polypeptides in vivo were shown to abrogen polypeptides and polymention provides freed tumour metastasis in 2 lung cancer models. The invention provides threat an angiogenesis-related disease or disorder, e.g. tumour metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, abrogen, kringle, hATF-kringle, angiogenesis, inhibitor, urokinase plasminogen activator, tumour, metastasis, cytostatic, gene therapy, gene; ss.
                                                                                                                                                                                                                   Sequence 258 BP; 62 A; 73 C; 72 G; 51 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human abrogen (hATF-kringle) coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New abrogen polypeptide, usefu:
diseases e.g. tumor metastasis
                                                                                                                                                                                                                                                                                                                                                                                                             ACC58336 standard; cDNA; 258
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Best Local Simi:
Matches 20;
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(first entry)

useful for treating an angiogenesis related

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Brockstedt

Fong TC,

codon"

/product= "Human abrogen" /note= "no start or stop

Location/Qualifiers

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partial/ 1. .258 /\*tag=

The present sequence is a coding sequence for a novel human abrogen, designated hATF-kringle, comprising the human urokinase plasminogen activator kringle domain. Abrogens such as hATF-kringle are potent inhibitors of endothelial proliferation and angiogenesis. Abrogen

Claim 32; Page 25; 95pp; English.

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Gaps

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Indels

Similarity 90.9%; Pred. No. 1.3e+02; 0.00 Conservative 0; Mismatches 2; Indels 0

0; Mismatches

56

CTGGAAGTCTGCCAGTGTCCTT

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polypoptides are capable of inhibiting or reducing cell proliferation induced by both basic fibroblast growth factor (bFGF) and vascular endothelial growth factor in a specific endothelial cell proliferation assay, vectors that expressed abrogen polypeptides in vivo were shown to reduce tumour metastasis in 2 lung cancer models. The invention provides abrogen polypeptides and polymorphotogen polypeptides and polymorphotogen polypeptides and polymorphotogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; utels contraction disorder; respiratory disease; male impotence; adult respiratory distress syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.
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include start and stop codon"
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                                                                                                                                                                                                            Score 18.8; DB 8; Length 258; Pred. No. 1.3e+02; O; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human urokinase-type plasminogen activator (uPA) kringle DNA.
                                                                                                                                                                             Sequence 258 BP; 62 A; 74 C; 72 G; 50 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human uPA
/note= "CDS does not
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                                                                                                                                                                                                            ch 72.3%;
1 Similarity 90.9%;
20, Conservative C
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*tag=
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P-PSDB; AAE16542.
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Human, urokinase-type plasminogen activator, uPA, therapy, hypertension, stroke, hypotension, atherosclerosis, heart attack, thrombotic disorder, stroke, hypotension, angiogenic disorder; pulmonary fibrosis, asthmatumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder; respiratory disease; adult respiratory distress syndrome, male impotence; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and anglogenic activity of a mammalian muscle, endchelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular
occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogensis, tumour cell metastassis, qlaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is human urokinase-type plasminogen activator (uPA) kringle DNA
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                                                                                                                                                                                                                                                   Match 72.3%; Score 18.8; DB 6; Length 264; Local Similarity 90.9%; Pred. No. 1.38+02; es 20; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                             Sequence 264 BP; 66 A; 74 C; 74 G; 50 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human uPA kringle and connecting peptide DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD27083 standard; DNA; 288 BP
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                   tumour cell
occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is a DNA encoding human urckinase-type plasminogen activator (UPA) kringle and connecting peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prourokinase mutant designed to acquire unique restriction sites.
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                                                                                                                                                                                          Score 18.8; DB 6; Length 288; Pred. No. 1.4e+02; 0; Mismatches 2; Indels C
                                                                                                                                                               Sequence 288 BP; 73 A; 84 C; 77 G; 54 T; 0 U; 0 Other;
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/note= "Wild-type= GC: Mutant= CA"
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note= "Wild-type= A: Mutant= G"
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/note= "Wild-type= T: Mutant=
209. .210
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                                                                                                                                                                                                                                                                                                                                                           AAN81299 standard; cDNA; 300 BP
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                                                                                                                                                                                             72.3%;
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(first entry)
                                                                                                                                                                                                            Local Similarity 90.9 es 20; Conservative
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P-PSDB; AAP80996.
                                                                                                                                                                                                          Similarity
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08-OCT-1990
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Site-directed mutagenesis creates two unique restriction sites, the first is recognised by SacI and the second by NdeI. The mutant sequence is inserted into an expression vector system for expression in eg E.coli. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                          Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; aethma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; adult respiratory distress syndrome; amino terminal fragment; ATF;
                                                                                                                                                                                                                                                                                                                     Human urokinase-type plasminogen activator amino terminal fragment DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Human uPA ATF"
|note= "CDS does not include start and stop codon"
                                                                                                    Score 18.8; DB 1; Length 300;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                          Sequence 300 BP; 77 A; 82 C; 75 G; 66 T; 0 U; 0 Other;
                                                                                                                                                                     CTGGAACTCTGCCACTGTCCTT 300
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ilarity 90.9%;
Conservative
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Human, urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; stroke; hypotension; asthma; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; adult respiratory distress syndrome; amino terminal fragment; ATF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atheroscierosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic
diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthmá, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is human urckinase-type plasminogen activator (uPA) amino terminal fragment (ATF) DNA
                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human uPA amino terminal fragment (ATF) and connecting peptide DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATF and connecting peptide" include start and stop codon"
                                                                                                                                                                                                                              Ö
                                                                                                                                                                                          Length 405;
                                                                                                                                                     Sequence 405 BP; 113 A; 105 C; 104 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                      72.3%; Score 18.8; DB 6; 90.9%; Pred. No. 1.4e+02; iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Human uPA
/note= "CDS does not
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                                                                                                                                                                                                                                                                                                                                                                                                 BD
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                                                                                                                                                                                                                                                                                                                                                                                             AAD27082 standard; DNA; 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                              Query Match 72.3
Best Local Similarity 90.9
Matches 20, Conservative
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The invention relates to a composition comprising one or more domains of uckinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endotherial cell or tissue. The composition is used for treating stroke, hyptotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell metastasis, glaucoma,

Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.

20-JUN-2000; 2000US-0212874P

(UYPE-) UNIV PENNSYLVANIA.

Cines DB, Higazi AA; WPI; 2002-122240/16.

P-PSDB; AAE16545

Claim 29; Fig 1M; 117pp; English

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disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, olotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is a DNA encoding human urokinase-type plasminogen activator (UPA) amino terminal fragment (ATF) and connecting peptide
   88888888888888
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Sequence 429 BP; 120 A; 115 C; 107 G; 87 T; 0 U; 0 Other;

Gaps . 0 Query Match 72.3%; Score 18.8; DB 6; Length 429; Best Local Similarity 90.9%; Pred. No. 1.4e+02; Matches 20; Conservative 0; Mismatches 2; Indels 0

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Search completed: February 19, 2004, 21:51:43 Job time: 25.0879 secs

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                                                                           February 19, 2004, 21:21:54; Search time 172.149 Seconds (without alignments) 4510.152 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES			ID		BX383606	BG178487	BQ053486	BQ054265
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ALS.1041 ALS.1041 ALS.1041 ALS.1041 ALS.204281 ALS.204281 ALS.204281 BB.10228158 BB.10228158 ACG1064 ACG1064 ACG1064 ACG1064 ACG10666 CCAS6282 BB.102282 CCAS6280 BB.102290 BB.102290 CCG56666 CCAS6282 CCG56666 CCG566666666666666666666666666	
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    1 CCTTCTGGAAGTCTGCCAGTGTCCTT
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Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG178487 178 bp mRNA linear EST 06-FEB-2001
602328305F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4429896 5',
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                                                                                /mol_type="mRNA"
/db_xref="taxon:960"
/db_xref="taxon:9001"
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/cell_the="JURKAT"
/cll_the="JURKAT"
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10-NORMALIZED"
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Mammaliai Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
                                                                                                                                                                                                                              /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.row: i column: 01
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Faraday Avenue Genoscope sequence ID : CSODJ013BF05QP1.
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100.0%; Score 26; DB 12; Length 778;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 26; Conservative 0; Mismatches 0; Indels
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                                                                 organism="Homo sapiens"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases I to 878)

NIH-MGC http://mgc.nci.nih.gov/.

Instinutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC. Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov

Plate: LLCM2122 row: 1 column: 06

High quality sequence stop: 394.
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BQ054265. GI:19813605
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/clone_moral inth MgC 106"
/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: Site_2:
/note_moral made by oligo-dr priming. Directionally cloned
into EcoR1/XhoI sites using the following 5' adaptor:
/gCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BQ053486
BQ053486
BY BP MRNA linear EST 29-MAR-2002
BQ080NOURT 6822017 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935253
BQ053486
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 986)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="natural killer cells, cell line"
/lab_host="DH10B_(phage_resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 878;
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AL541041 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE005YK23 5-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dI) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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1 (1808-81 to 1201)

11, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

On Peb 15, 2001

On Peb 15, 2001 this sequence version replaced gi:12871733.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 FWTX cedex - France
BP 191 91006 FWTX cedex - France
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9825.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgi-bin/cluster.cgi?sec=CSODE005AF12QP1&cluster=9825.r. Contact Feng Liang Email : fliang@lifetech.com URL : http://fullength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODE005AF12QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 12; Length 1020;
Pred. No. 1.6;
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100.0%; Pred. No. ..
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AL541041.2 GI:30544829
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Best Local Similarity 100.
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC lob"
/note="Organ: blood; Vector: pOTB7; Site_1: Xho1; Site_2:
SooR1: cDNA made by oligo-dr priming. Directionally cloned
into BCoRI/Xho1 sites using the following 5' adaptor:
GGGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGENCOURT_6830234 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936362 5', mRNA sequence.
BQ054281
BQ054281.1 GI:19813621
EST.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1020)
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                                                                                                                    Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2155 row: i column: 12
High quality sequence stop: 515.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
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    1020
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                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Matches 26; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

MEDLINE PUBMED COMMENT

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RESULT 7 BM483329/c

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oilgonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                  1 (bases 1 to 389)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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480839 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BI898999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0453 row: M column: 21
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0453M21"
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Location/Qualifiers
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Unpublished (2000)
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Bos taurus (
Bos taurus
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Best Local Similarity
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84112, USA
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BI898999/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: Text of a mithdemail marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
V0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGARACGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ620995 13-DEC-2000 1M0453M21R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0453M21 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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/note:-pcMV SPORT6; Site
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1 (bases 1 to 354)
Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wary, J.E., White, J., Cho, J., Fabrrankrug, S.C., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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                                                                                                                                                                                                                                    BM483329 3BOV BOS taurus CDNA 5', mRNA sequence.
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4356
Fax: 402 762 4399
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92.0%; Pred. No. 72;
tive 0; Mismatches
337 CCTTCTGGAAGTCTGCCAGTGTCCTT 312
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Plate: 6 'row: C column: 14
Seg primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
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AZ620995.1 GI:11743185
GSS.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                          BM483329
BM483329,1 GI:18533657
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Best Local Similarity
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source

FEATURES

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RESULT 8 AZ620995 LOCUS DEFINITION

Matches

ACCESSION VERSION KEYWORDS SOURCE

us-09-939-853a-141.rst

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Query Match Best Local Similarity Matches 22; Conserv
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BB468570/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                     Tel: 402 762 4366

Fax: 402 762 4366

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

VO.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 bp mRNA linear EST 08-FEB-2001
mac35e07.x1 Soares mouse 3NbNS Mus musculus cDNA clone
BG228158
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                              Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Haeton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pcMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Gappbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1499500
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                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC_2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 105 row: P column: 20
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9913"
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Mus musculus
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PCR PRimers
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                                                                  (bases 1 to 541)
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Unpublished (1997)
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BG228158/c
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VERSION
KEYWORDS
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sayauki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., et al. 2001)

I. Unpublished (2001)

On Jul 22, 2000 this sequence version replaced gi:9385759.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninol,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs.to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
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llarity 88.0%; Pred. No. 3.8e+02;
Conservative 0; Mismatches 3;
                                                                                                                                                                         organism="Mus musculus"
High quality sequence stop: 402.
Location/Qualifiers
                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4001772"
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contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGACACTCGAGTTTTTTTTTTTTTVV 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB195256 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330087124 3', mRNA sequence.
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                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site 1: Sal1; Site_2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
                                                                                                                     10 (11), 1757-1771 (2000)

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Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,

Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with
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/dev_stage="12 days embryo"
/lab.host="DH108"
/clone_lib="RIKEN full-length enriched, 12 days embryo
eyeball"
                                                                                                                                                                                                                                                                                                                                                                                                                           Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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Location/Qualifiers
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Hara, A., Hiramoto, K., Hori, F., Ishli, Y., Ito, M., Kawai, J., Konda, M., Kondo, H., Kodda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shizaki, T., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takada, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. Riken Mouse BSTs (Arakawa, T., et al. 2001)

J. Unpublished (2001)

J. On Jun 30, 2000 this sequence version replaced gi:8855875.

Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)

1.7-22, Suchiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,X.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Chara,E., Matsuliki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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further details.
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/clone="A330087124"
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Mus musculus 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2510040D07 product:hypothetical Signal peptidase/Trp-Asp (WD) repeats profile/Trp-Asp (WD) repeats full insert sequence.
3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 1226)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                  77.7%; Score 20.2; DB 10;
88.0%; Pred. No. 4.5e+02;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Saio,H., Saito,H., Saito,R., Sakai,C., Sakai,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,Y., Sano,H., Sasaki,D., Shibata,X., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission

Li Submitted (10-UID-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Physical-45-53-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/strain="CS7BL/6J"
/db xref="RANTOM DB:210040D07"
/db xref="Mol:1902545"
/db xref="Mol:1902545"
/db xref="Hol:1902545"
/db xref="Mol:1902545"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/do gragge="13 days embryo"
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KLGHYQLHQHAANNLSFHPSGNYLITASSBSTLKILDLMEGRLLYTLHGHQGPATTV
AFSRTGEXFASGGSDGVMVWKSNFDIVDYGDMKARRPPPLTSSSGTLTVSILBGRLI
LTEDRLKQCLENQQLIMQRTPP"
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WHMKPQSRAYRFTGHNDAVTCVNFSPSGHLLASGSRDKTVRIWVPNVKGBSTVFRAHT
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ACCESSION VERSION KEYWORDS SOURCE

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Encyclopedia Project of Genome Exploration Research Group in Rikk
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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|clone="0STS861#"
|clone="type="embryonic stem cell"
|clone=lib="mus musculus 1298v/Ev"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Okazaki in and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                   HTC 19-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 3016)
                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     he RIKEN Genome Exploration Research Group Phase II Team and the
                                                 Mus musculus adult male spinal cord CDNA, RIKEN full-length enriched library, clone:A330087124 product:unclassifiable, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                           AK039689.1 GI:26087341
HTC; CAP trapper.
Mus musculus (house mouse)
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         RESULT 14
AK039689/c
LOCUS
DEFINITION
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JOURNAL
                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOUÈNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
PUBMED
REFERENCE
AUTHORS
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AUTHORS
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MEDLINE
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AUTHORS
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TITLE JOURNAL

PUBMED

TITLE

REFERENCE AUTHORS AUTHORS

COMMENT

JOURNAL REFERENCE

TITLE

MEDLINE PUBMED

JOURNAL

TITLE

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Mus musculus (house mouse)

Mus musculus (house mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (Dases 1 to 276)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.;

Piggott,J., BeltrandelRio,H., Buxton,B.C., Edwards,J., Finch,R.A., Friddle,C.J. Gupta,A., Hansen,G., Hu,Y., Hunng,W., Jaing,C., Rey,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qan,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhors,II., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

Wnkl kinase deficiency lowers blood pressure in mice a gene-trap screen to identify potential targets for therapeutic intervention proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUSUBLES 276 bp DNA linear GSS 01-OCT-2003 OST58614 Mus musculus 1298v/Ev Mus musculus genomic clone OST58614, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="spinal cord"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
1. 3016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3016;
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prepare mouse tissues.
Please visit our web site for further details.
URL:http://gnome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                1. 3016

/organism="Mus musculus"

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/clone="A330087124"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20.2; DB 11,
Pred. No. 7.6e+02;
0; Mismatches 3;
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ORIGIN

Query Match 76.2%; Score 19.8; DB 29; Length 276; Best Local Similarity 84.0%; Pred. No. 4.8e+02; Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps

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2 CTTCTGGAAGTCTGCCAGTGTCCTT 26

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Search completed: February 20, 2004, 01:41:40 Job time: 176.149 secs

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LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 97, Appl
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 927, App
Patent No. 5219569
                                                                             February 19, 2004, 21:32:00; Search time 4.21902 Seconds (without alignments) 3419.919 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 95, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Patent No.
Sequence 1
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. /GGTZ_6/ptodata/2/ina/5A_COMB.seq:*
.: /GGTZ_6/ptodata/2/ina/5B_COMB.seq:*
.: /GGTZ_6/ptodata/2/ina/6A_COMB.seq:*
.: /GGTZ_6/ptodata/2/ina/6B_COMB.seq:*
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.: /GGTZ_6/ptodata/2/ina/PGTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-101-272G-95
US-09-101-272G-95
US-09-101-272G-97
US-08-254-922-1
US-08-286-748B-1
US-08-153-799-17
US-08-153-799-17
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-09-542-615A-122
-09-606-421B-122
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-09-542-615A-123
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US-09-562-702A-9
US-09-313-294A-38
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Maximum Match 100%
Listing first 45 summaries
                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length DB
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Maximum DB seq
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Sequence 25, Appli Sequence 2, Appli Sequence 1335, Ap Sequence 1584, Ap Sequence 285, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 5, Appli Sequence 5, Appli Sequence 25, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	Sequence 5, Appli
9-800-1274-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9	US-08-487-797-5
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Sequence 11, Application US/08797689
Patent No. 587569
Ratent No. 1875669
GENERAL INFORMATION:
APPLICANT: Fleer, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Veh, Patrice
TILLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: ONVEL BIOLOGICALLY ACTIVE POLYPEPTIDES
TITLE OF INVENTION: ONVEL BIOLOGICALLY ACTIVE POLYPEPTIDES
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRESSEE: ANDRESSEE: ADDRESSEE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUNTRY: USA

CUNTRY: USA

ZIP: 1942-6

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING STEM: System 7.1

SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAA-1997
CLASSIFICATION: 435
PILING DATE: 28-JUL-1997
APPLICATION NUMBER: WS 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JAA-1993
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JAA-1993
ATTORNEY/AGENT INFORMATION:
NAMM: Smith Ph.D. JULIE K.
REGISTRATION WUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELEPHONE: (610) 454-3899
INFORMATION FOR SEQ ID NO: 11:
FELEPHONE: (610) 454-3899
INFORMATION FOR SEQ ID NO: 11:
FELEPAX: CRIPE PAIRSITICS:
ALIGNMENTS
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STREET: 500 Arcola Road, 3C43
CITY: Collegeville
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Gaps
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                                                                                                                                                                                                                                                                      Sequence 7.2. Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: NISSIN FOOD Products Co., Ltd.
APPLICANT: NISSIN FOOD PRODUCTS CO., Ltd.
TITLE OF INVENTION: CANCERCUS METASTASIS INHIBITOR
FILE REFERENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR APPLICATION NUMBER: J996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SEQ ID NO 7.2
LENGTH: 600
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Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT PILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: UF 1059/1996
PRIOR PILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Version 3.1
SEQ ID NO 79
LENGTH: 624
TYPE: DAM
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                             Query Match 72.3%; Score 18.8; I Best Local Similarity 90.9%; Pred. No. 11; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: ATFHI chimeric protein NAME/KEY: CDS (12)...(593) COTATION: (12)...(593) CTHER INFORMATION: NAME/KEY: mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.8;
Pred. No. 1
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FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: ATF domain of uPA

NAME/KEY: CDS

LOCATION: (1)..(600)

OTHER INFORMATION:

NAME/KEY: mat peptide

LOCATION: (61)..()

OTHER INFORMATION:

US-09-101-272G-72
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Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    RESULT 3
US-09-101-272G-72
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US-09-101-272G-79
    US-09-984-186-11
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Petent No. 6686179

GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard

APPLICANT: Fleer, Alain

Guitcon, Jean-Dominique

Jung, Gerard

Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,

CONTAINING SAID POLYPEPTIDES

CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                             .
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                                                                                                                                                     Length 423;
                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURREY APPLICATION DATA:
PLING DATE: 29-Oct-2001
CLASSIFICATION: COMPUTER: US/OS/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: CURROWN>
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APPLICATION NUMBER: US/08/797,689
FILING DATE: 31.-AN-11997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28.-UL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31.-AN-1992
APPLICATION NUMBER: PCT/FK93/00085
FILING DATE: 28.-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                Score 18.8; D
Pred. No. 11,
0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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                                                                                                                                                                                                                                    5 CTGGAAGTCTGCCAGTGTCCTT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (610) 4:
INFORMATION FOR SEQ ID NO:
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TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                   3..419
                                        FEATURE:
NAME/KEY: CDS
LOCATION: 3..4
US-08-797-689-11
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                                                                                                                       Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICAMY: Victor Gurewich
TITLE OF INVENTION: USE OF INTRA-PLATELET
TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN
TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN
TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN
TITLE OF INVENTION: INHIBITION OF THROMBOSIS
NUMBER OF SEQUENCES: I
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Mesachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER. READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: MordPerfect (Version 5.0)
SOFTWARE: MordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,922
FILING DATE: June 7, 1994
CLASSIFCATION: 424
PRIOR APPLICATION NUMBER: 08/014,207 -
RILING DATE: February 5, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.3%; Score 18.8; I Best Local Similarity 90.9%; Pred. No. 14; Matches 20; Conservative 0; Mismatches
                                                                                                                       Query Match 72.3%; Score 18.8; I
Best Local Similarity 90.9%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: J. Peter Fasse
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04353/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                        233 cregaacrereceacrererr 254
                                                                                                                                                                                                                           5 CTGGAAGTCTGCCAGTGTCCTT 26
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                                                                                                                                                                                                                                                                                                                                                                          US-08-254-922-1; Sequence 1, Application US/08254922; Patent No. 5626841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
NAME/KEY: mat_peptide;

LOCATION: (15)..()

CTHER INFORMATION:

US-09-101-272G-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-286-748B-1
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                                                                                                    DB 4; Length 624;
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72.3%; Score 18.8; DB 4; Length 645;
Best Local Similarity 90.9%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97, Application US/09101272G;
Patent No. 6509445;
GENERAL INFORMATION:
ATTLE OF INTERNATION: CANCEROUS METASTASIS INHIBITOR FILE REFERENCE: 050979
FILE REFERENCE: 050979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1008-07-08
NUMBER OF SEQ ID NOSS: 107
SOFTWARE: Patentin version 3.1
SEQ ID NO 97
LENGTH: 666
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                  RESULT 5
(US-00-101-272G-95)
(US-00-101-272G-95)
(US-00-101-272G-95)
(US-00-101-272G-95)
(US-00-101-272G-95)
(US-00-101-272G-95)
(US-00-101-272G-95)
(US-00-101-272G-95)
(URABLI REPRENDEN CANCEROUS METASTASIS INHIBITOR FILLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR FILLE REPRENDEN CANCEROUS METASTASIS INHIBITOR FILLE REPRENDEN CANCEROUS METASTASIS INHIBITOR FILLE REPRENDEN CANCEROUS METASTASIS INHIBITOR FILLE REPRENDENT ON NUMBER: US/09/101,272G
(URRENT FILING DATE: 1998-07-08)
(UNMBER OF SEQ ID NOS: 107)
(SOFTWARE: PAUGHLIN VERSION 3.1)
(SOFTWARE: PAUGHLIN VERSION 3.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: ATFHI-CL chimeric protein
NAME/KEY: CDS
LOCATION: (12). (614)
CTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: (15). ()
LOCATION: (15). ()
COTHER INFORMATION:
US-09-101-272G-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE:
OTHER INFORMATION: ATFHI-ML chimeric protein
LOCATION: (12) .. (635)
                                                                                                 72.3%; Score 18.8; D
90.9%; Pred. No. 12;
iive 0; Mismatches
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                                                                                                                                                                                                   S CTGGAAGTCTGCCAGTGTCCTT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                 Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (12)..(635)
OTHER INFORMATION:
; LOCATION: (15)..(); OTHER INFORMATION: US-09-101-272G-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-101-272G-97
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Query Match 72.3%; Score 18.8; Dest Local Similarity 90.9%; Pred. No. 14; Matches 20; Conservative 0; Mismatches
                   PRILICATION: 06-OCT-13>2
CLASSIPTCATION: 435
CLASSIPTCATION: 435
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION WIDBER: 10 20025
FILING DATE: 07-OCT-1991
FLICOMMUNICATION INFORMATION:
TELEFAX: (202)293-766
TELEFAX: (202)293-766
TELEFAX: 6491103
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1236 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT IRFORMATION:
NAME: SWOPE, R HAIN
оныык: US/07/957,039A
06-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 credaacrcreccacrercrr 240
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: human
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: CDS
.) LOCATION: 1..1
US-07-957-039A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
          APPLICANT: VICTOR GUREWICH
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.3%; Score 18.8; DB 1; Length 1233; 90.9%; Pred. No. 14; tive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/07957039A

Patent No. 5389538
GENERAL INFORMATION:
APPLICANT: TANABE, TOSHIZUMI
APPLICANT: HIROSE, MASANCI
APPLICANT: HIROSE, MASANCI
APPLICANT: MASUO
ITLE OF INVENTION: MUTANT HUMAN PROUROKINASE
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSER: Sughrue, Mion, Zinn, Macpeak & Seas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 02110-2804
COMUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DIATA:
APPLICATION NUMBER: US/08/286,748B
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DAIN;

APPLICATION NUMBER: US/08/286,748B
FILLING DATE: ANGURE 5, 1994
CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY-AGENT INFORMATION:
NAME: J. Beter Fasse
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 32,983
REGISTRATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 credakcrcreckerererer 240
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
SDNESS: single
SY: linear
                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                         Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-07-957-039A-7
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Gaps
                                        0
Length 1236;
                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHILL Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
                                                                                                                                                                                                                                    Sequence 17, Application US/08153799
Patent No. 576683
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karren J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUTICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 927:
SEQUENCE CHARACTERISTICS:
LENGTH: 1236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 credaacrereceaererer 240
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Patent No. 6426072
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Tongtong
Fan, Liqun
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky, Yasir A.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                             CLONE: GENBANK
CLONE: 91311467
US-09-023-655-927
                                                                                                                                                                                                                                                                 TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:1:
; LENGTH: 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-643-597-122
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Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Goods, Benjamin G.
APPLICANT: Goods, Benjamin G.
APPLICANT: Jeffrey J. Seilhamer
ITILE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
ITILE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS: 1508
CORRESPONDENCE ADDRESS: 1508
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..1236
OTHER INFORMATION: /function= "human mature
OTHER INFORMATION: urokinase-type plasminogen activator (uPA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
72.3%; Score 18.8; DB 1; Length 1236;
Best Local Similarity 90.9%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: primer_bind
LOCATION: 13..47
OTHER INFORMATION: /standard_name= "PCR primer binding
OTHER INFORMATION: site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: primer_bind

LOCATION: 376..418

OTHER INFORMATION: /standard_name= "PCR primer binding
US-08-153-799-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TRYER Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 chádaachcháccachchhir
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 921832
TELECOMMUNICATION INFORMATION:
TELEFRONE: (908) 655 2400
TELEFAX: (908) 771 6159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 CTGGAAGTCTGCCAGTGTCCTT 26
                                                                      TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR ENQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1236 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-023-655-927
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Ouery Match 72.3%; Score 18.8; DB 4; Length 1236; Best Local Similarity 90.9%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 2; Indels 0
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APPLICANT: MONGIL, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455011
                                                                                                                                                                                                                                                                  5219569-1; Patent No. 5219569
APPLICANT: BLABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
                                                                                                                                                                                                                                                                                                                                          GORDON A.
TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,858
FILING DATE: 16-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 725,468
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US-09-542-615A-122

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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEC ID NOS: 350
SOFTWARE: FactSEQ for Windows Version 3.0
SEQ ID NO 122
LENGTH: 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.4556
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1475
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SEQ ID NO 122
LENGTH: 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-480-884A-122
; Sequence 122, Application US/09480884A
; Parent No. 6482597
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Bangur, Chaitanya S.
Hosken, Nancy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang, Tongtong
Fan, Liqun
                                                                                                                                            TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
; ORGANISM: Homo sapien
US-09-480-884A-122
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Wang, TO
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Query Match

Dest Local Similarity 90.9%; Pred. No. 14;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps

Qy 5 CTGGAAGTCTCCCAGTGTCCT 26

Db 359 CTGGAACTCTCCCAGTCCTT 380
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Search completed: February 20, 2004, 01:45:11 Job time : 6.21902 secs

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Sequence 951, App
Sequence 953, App
Sequence 21302, A
Sequence 195852,
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
                                                                                                                         February 19, 2004, 23:23:34 ; Search time 62.4956 Seconds (without alignments) 1456.787 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 26, F
Sequence 18, Ag
Sequence 13, Ag
Sequence 11, Ag
Sequence 11, Ag
Sequence 11, Ag
Sequence 11, Ag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Ggn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/ Ggn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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/ Ggn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-867-550-953
US-09-867-550-953
US-10-027-632-195852
US-10-233-675A-6
S US-10-233-675A-6
S US-10-233-675A-28
US-10-233-675A-28
US-09-880-503-10
US-09-880-503-11
US-09-880-503-13
US-09-880-503-14
US-09-984-18-11
US-09-984-18-11
US-10-237-667-11
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                                                                                                                                                                                                                                                                                                                                                                              2308684 segs, 1750822206 residues
                                                                                                                                                                                                                 US-09-939-853A-141
26
1 ccttctggaagtctgccagtgtcctt 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                         IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
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Perfect score:
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Maximum DB seq
                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                Run on:
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11	7:	Semience 11, Appl	equence 581	15,	12,	e 1,	۲,	122	122	Sequence 122, App	12	e 12	15	e 12	22	'n	123	equence 123	123	e 12	12	12	18	16	41	10	12	34
US-10-237-866-1	4 US-10-237-871	11S-09-890-	US-09-917-800A-	US-09-880-503-1	-60-SN	5 US-10-407-821-	급	US-09-735-705-12		US-09-897-778-12	US-09-466-39	US-10-117-982-12	US-10-101	0-313-986-12	4 US-10-131-985-2	US-10-401-07	US-09-735-705-	-850-71	US-09-897-778-1	US-09-466-396A-1	14 US-10-117-982-123	US-10-313-986-12	US-10-171-311-1	US-10-301-822-16	US-10-295-027-41	us	US-10-159-563-12	14 US-10-247-671-34
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## ALIGNMENTS

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| Fatent No. Uszuuzuo82206A1
| GENERAL INFORMATION:
| APPLICANT: Leach, Martin D.
| APPLICANT: Mehraban, Fuad,
| APPLICANT: Mehraban, Fuad,
| APPLICANT: Topper, Jamela
| APPLICANT: Topper, Jamela
| APPLICANT: Topper, Jamela
| APPLICANT: Topper, Jamela
| APPLICANT: Topper, Jamela
| APPLICANT: Topper, Jamela
| TITLE OF INVENTION: No. US2002082206A1e1 Polynucleotides from Atherogenic Cells and I
| TITLE OF INVENTION: Thereby
| FILE REFERENCE: 21402-013 (Cura-313)
| CURRENT APPLICATION NUMBER: US/09/867,550
| PRIOR FILING DATE: 2001-09-20
| PRIOR FILING DATE: 2000-05-30
| NUMBER OF SEQ ID NOS: 2125
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 951
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US-09-867-550-953/c
Sequence 953, Application US/09867550
; Patent No. US20020082206A1
                     Sequence 951, Application US/09867550 Patent No. US20020082206A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-09-867-550-951
JS-09-867-550-951/c
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GENERAL INFORMATION:

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APPLICANT: Neebit, Mark
APPLICANT: Neebit, Mark
APPLICANT: Neebit, Mark
APPLICANT: Pong, Timochy
APPLICANT: Brockstedt, Dirk
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
TITLE OF INVENTION: Them To Inhibit Anglogenesis
FILE REFERENCE: $7010.27
CURRENT APPLICATION NUMBER: US/10/233,675A
CURRENT PILING DATE: 2002-09-04
PRIOR FILING DATE: 2001-09-04
                                                                                                                                                                                                                                                                                        FILE OF INVENTION: 10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01/10-01
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Pred. No. 5.9;
0; Mismatches
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; OTHER INFORMATION: human derived abrogen
US-10-233-675A-2
                                                                                                                                                                                     Sequence 195852, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CTICIGGAAGICIGCCAGIGIC 23
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90.9%;
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1 Similarity 95.5%;
21; Conservative (
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 258
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
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US-10-027-632-195852
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SEQ ID NO 195852
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US-10-233-675A-2
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                APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REPERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
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Fublication No. US20030165831A1
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Fublication North Carles
Fublication Number: US/09/814,353
FURRENT APPLICATION NUMBER: US/09/814,353
FURRENT APPLICATION NUMBER: US 60/191,031
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-06-15
FRIOR FULING DATE: 2000-06-15
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100.0%; Pred. No. 0.013;
live 0; Mismatches 0;
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100.0%; Score 26;
Best Local Similarity 100.0%; Pred. No.
Matches 26; Conservative 0; Mismatch
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SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 953
LENGTH: 763
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21302
LENGTH: 864
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US-09-814-353-21302
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Best Local Similarity 100.(
Matches 26; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Gaps . 0

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Sequence 26, Application US/10233675A
; Sequence 26, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
    APPLICANT: Nesbit, Mark
; APPLICANT: Fong, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, Timoch, 
                                                                                     Sequence 23, Application US/10233675A
Publication No. US20030228298A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nesbit, Mark
APPLICANT: Brockstedt, Dirk
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for TITLE OF INVENTION: Them To Inhabit Angiogenesis
FILE REFERENCE: ST01027
CURRENT PELING DATE: 2002-09-04
FRIOR APPLICATION NUMBER: 6/316,300
FRIOR APPLICATION NUMBER: 6/316,300
FRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 90.9%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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OTHER INFORMATION: n = a or
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Best Local Similarity
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US-10-233-675A-26
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LENGTH: 258
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APPLICANT: Nesbit, Mark
APPLICANT: Nosbit, Mark
APPLICANT: Frong, Timothy
TITLE OF INVESTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
TITLE OF INVENTION: Them To Inhibit Angiogenesis
FILE REPERENCE: STOLO27
CURRENT APPLICATION NUMBER: US/10/233,675A
CURRENT APPLICATION NUMBER: 00/316,300
PRIOR APPLICATION NUMBER: 00/316,300
PRIOR PLING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO B
LENGTH: 258
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0; Mismatches
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Pred. No. 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: human derived abrogen US-10-233-675A-6
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                                                                                                                                                                                                                                                   Sequence 6, Application US/10233675A Publication No. US20030228298A1 GENERAL INFORMATION:
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                                                         5 CTGGAAGTCTGCCAGTGTCCTT
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Best Local Similarity 90.9%;
Matches 20; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
20; Conservative
                                                                                                                                                                                                                        10-233-675A-6
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Matches
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REFERENCE/DOCKET NUMBER: ST92006-US TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                    Score 18.8;
Pred. No. 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Smith Ph.D., Julie K. REGISTRATION NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 cresaAcrereceacrererr 240
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09984186
Patent No. US20020151011A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                 72.3%;
                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-880-503-13
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Best Local Similarity
Matches 20; Conserva
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US-09-984-186-11
                                                                                                                                                                             SEQ ID NO 13
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| Sequence 18, Application US/09880503
| Sequence 18, Application US/09880503
| Sequence 18, Application US/09880503
| APPLICANT: CINES, Douglas B
| APPLICANT: HIGAZI, Abd Al-Roof
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND FILE REFERENCE: 9596-331
| CURRENT PLILIGATION NUMBER: US/09/880,503 | CURRENT APPLICATION NUMBER: US 60/212,847 | PRIOR APPLICATION NUMBER: US 60/212,847 | PRIOR PLILING DATE: 2000-06-20 | NUMBER OF SEQ ID NOS: 18 | SEQ ID NOS: 18 | SEQ ID NO 18 | LENGTH: 288 | LENGTH: 288
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                                                                                                                                                  APPLICANT: CINES, DOUGLAS B
APPLICANT: CINES, DOUGLAS B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT PILING DATE: 2001-06-13
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 10
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0; Mismatches
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US-09-880-503-13
Sequence 13, Application US/09880503;
Patent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 chégaachchéccachchrig
78 credaacrefeccacrefectr 99
                                                                                                         Sequence 10, Application US/09880503
Patent No. US20020131964A1
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CORGANISM: Homo sapiens
US-09-880-503-18
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US-09-880-503-10
                                                                                          US-09-880-503-10
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AND PHARMACEUTICAL COMPOSITION
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TILLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct_2001
CLASSIFICATION PATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: WS 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: RP 92/01064
FILING DATE: 31-JAN 1992
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JUL-1994
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Gaps

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Length 423; Indels

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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES
                                                                                                                                                 DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Mord 5.1 (Patentin)
CURRENT APPLICATION DATA: 10.237,708
FILING DATE: 10.56p-2002
CLASSIFICATION: CUNROWN:
PRIOR APPLICATION NUMBER: US/08/797,689
FILING DATE: 31.34A-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31.34A-1994
APPLICATION NUMBER: PS 2/01064
FILING DATE: 32-ULL-1994
APPLICATION NUMBER: PS 2/01064
FILING DATE: 32-ULL-1994
APPLICATION NUMBER: PS 7/01064
FILING DATE: 28-ULL-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMITH Ph. D., Julla K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: S-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
RADAESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-237-708-11
Sequence 11, Application US/10237708
Publication No. US20030036170A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Guitton, Jean-Dominique
Jung, Gerard
Weh, Patrice
Yeh, Patrice
Yeh, Patrice
                                                                                                                                            72.3%; Score 18.8; I 90.9%; Pred. No. 34; cive 0; Mismatches
                                                    ) LOCATION: 3..419
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-237-667-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 3..419
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-237-708-11
                                                                                                                                                                                                                                                                             230 creda Acrerece acrerer 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: (610) 454-3839 (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: (610) 454-383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
                                                                                                                                          Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                    5 CTGGAAGTCTGCCAG1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PA
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                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                              Query Match 72.3%; Score 18.8; DB 9; Length 423; Best Local Similarity 90.9%; Pred. No. 34; Matches 20; Conservative 0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Macincosh
COERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,667
FILING DATE: 10-Sep-2002
CLASSIFICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN.1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN.1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 23-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 23-JAN.1992
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JAN.1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3809
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Rhone-Poulenc Rorer Inc. STREET: 500 Arcola Road, 3C43 CITY. Collegeville STATE: PA COUNTRY: USA
                                                                                                                                          ; LOCATION: 3..419
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-984-186-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-237-667-11
Sequence 11, Application US/10237667
Publication No US20030022308A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Allain
                                                                                                                                                                                                                                                                                                                                                                                    230 crecaacrereceacrerer 251
                                                                                                                                                                                                                                                                                                                                           5 CTGGAAGTCTGCCAGTGTCCTT 26
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                       NAME/KEY:
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Query Match
72.3%; Score 18.8; DB 14; Length 423;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps

S CTGGAAGTCTGCCAGTGTCCTT 26

à q Search completed: February 20, 2004, 05:59:21 Job time : 64.4956 secs

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February 19, 2004, 21:21:18 ; Search time 96.3181 Seconds (without alignments) 9899.970 Million cell updates/sec
                                                                                                                                                                                                                                     6940544
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                        3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                  US-09-939-853A-142
22
1 tgagaggttctgggtgtccta 22
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Maximum Match 100%
Listing first 45 summaries
                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                      Scoring table:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description:	AX443201 Sequence AX443133 Sequence AX443135 Sequence BCC42041 Homo sapi AX452880 Sequence AX780857 Sequence AX780857 Sequence AX780857 Sequence AX780857 Sequence	ACUSESS HOME SAPI CONTINUATION (3 of ACUSESS HOME SAPI ACUSESS HOME SAPI ACUSES TORSOPHII ACUSES HOME SAPI ACUSES HOME SAPI	ABO03512 Drosophil ABJ2847 Mususe DNA AC120340 Mus muscu AC120340 Mus muscu AC12554 Mus muscu AC124515 Mus muscu AC132376 Mus muscu AC132376 Mus muscu AC132376 Mus muscu AC132376 Mus muscu AC132376 Human DNA AC004899 Homo sapi AC004899 Homo sapi AC004899 Homo sapi AC01656 Homo sapi AC139753 Mus muscu AC139753 Mus muscu AC12676 Homo sapi AC12676 Homo sapi AC12676 Homo sapi AC12678 Mus muscu AL26823 Mus muscu AL26823 Mus muscu AL26823 Mus muscu AL26823 Mus muscu AL26823 Mus muscu AL26823 Mus muscu AL26823 Mus muscu AL26823 Mus muscu AL26823 Mus muscu AL28898 Rattus no AL20899 Rattus no AL20899 Rattus no AL20899 Rattus no AL20899 Rattus no AL20899 Rattus no AL20899 Mus muscu AL28950 Homo sapi	Hart,M., Kekuda,R., ., Tomlinson,J.E.,
SUMMARIES. DB ID	AX44 AX444 BC045 AX78 AX78 AX78 AX78 AX78 AX78	A A COOLING A A COOLING A A COOLING A A COOLING A A COOLING A COOL	3 AE003312 10 AL228947 2 AC120340 2 AC120340 2 AC120340 2 AC122504 2 AC124033 3 AK132376 3 AK132376 5 AX834238 6 AX834238 6 AX834238 6 AX834238 6 AX834238 5 AL59402 9 AC01412 2 AC01412 2 AC016412 2 AC016412 2 AC016676 10 AC126899 10 AL668823 2 AC016676 10 AC126899 10 AL668823 2 AC016676 10 AC126899 2 AC128996 9 AX129950 2 AC126899 9 AC026671 10 AL668823 2 AC016676 10 AC126676 10 AC126676 10 AC126679 2 AC126999 9 AC016676 10 AC126679 10 AC126899 9 AC016676 10 AC126679 10 AC126699 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC126999 10 AC1269999 10 AC1269999 10 AC126999999999999999999999999999999999999	Y, P.B., Grosse, W.M., ek, K.A., Szekeres, E.S g, R.B. c acids encoding same
% Query ore Match Length	000000000000000000000000000000000000000	9.4 4 88 8.2 11009 9.4 8 88 8.2 11009 9.4 8 88 8.2 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 88.5 1200 9.4 8 98.5 1200 9.4 8	8.8 8.8 8.8 8.8 8.4 8.4 8.4 1 10.4 10.4 10.4 10.4 10.4 10.4 10.4	1 Burgess, C.E., Conl Shimkets, R.A., Spy Topper, J.N. and Ya Proteins and nucle
Result No. Sci	. O O	08798888696 0879888888888		REFERENCE AUTHORS TITLE

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 88 Row: a Column: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens (human)
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                                                                                                                  Similarity
22; Conserv
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Best Local S:
Matches 22,
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
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REFERENCE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Propper, J.N. and Yang, R.B.
Proteins and Constant acids encoding same
Patent: WO 0216599-A 74 28-FEB-2002;
Curagen Corporation (US); COR THERAPEUTICS, INC. (US)
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Protetins and mucleic acids encoding same Patent: WO 0216599-A 76 28-FEB-2002;
Curagen Corporation (US); COR THERAPEUTICS, INC. (US) 1.1183
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Patent: WO 0216599-A 142 28-FEB-2002;
Curagen Corporation (US) ; COR THERAPEUTICS, INC. (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Score 22; DB 6; Length 1183;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                         /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="oligonuclectide primer"
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AX443135
AX443135.1 GI:21690556
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Sequence 74 from Patent W00216599.
AX443133
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1. (Dases I to 2518)

Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Schetz, T.E., Scares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Rah, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Modan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Broc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Neb site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
B.K. M. Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear PRI 07-OCT-200 transcript variant 1, mRNA (cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2538)
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Submitted (13-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                              100.0%; Score 22; DB 6; Length 1183; larity 100.0%; Pred. No. 0.36; Conservative 0; Mismatches 0; Indels
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Homo sapiens Src-like-adaptor 2, transcript v clone MGC:49845 IMAGE:4429896), complete cds.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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BC042041.1 GI:27469842
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us-09-939-853a-142.rge

FEATURES

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Human DNA sequence from clone RP3-460JB on chromosome 20g11.21-11.23 Contains the 3' end of the gene for a novel protein similar to N-myc downstream regulated (NDRG1) the 5' end of a gene encoding a novel protein tyrosine kinase, BSTs, STSs and GSSS,
                                                                                                                                                                                                                                                                                                                                                       PAT 14-JUL-2003
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On Aug 7, 2000 this sequence version replaced gi:6425549.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone are annotated as variations variation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 66741)
Skuce,C.
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Novel genetic markers for leukemias
Patent: WO 03039413-A 3014 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universiteet Muenchen (DE);
PD Dr. Dr. (DE); Schoch, Claudia (DE);
Location/Qualifiers
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                                                                                                             0.38;
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                                                                              Query Match
100.0%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 22; Conservative 0; Mismatches
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AL031662.26 GI:9716901
HTG; NDRG1; SH2 domain.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.0%; Pr
Matches 22; Conservative 0;
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AGGPAELSLAGEPTITUSEGGDWWTVLSFVSGREYNIPSYHYRIHGLDNGWLYE
RAEELILLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHGLDNGWLYE
SPRLTPPSLQALVDHYSELADDICCLIKEPCYLQBAGPLPGKDIPLPVTVQRTPLNWK
SLDSSLLFSSRAATGBESLLSEGGLRESLSFYISLNDBAVSLDDA"
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28416422. Location/Qualifiers
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/note="SH3; Region: SH3 domain. SH3 (Src homology 3)
domains are often indicative of a protein.involved in
signal transduction related to cytoskeletal organization.
First described in the Src cytoplasmic tyrosine kinase.
/db xref="CDD:pfamo0018"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       642. .890
/note="SH2; Region: SH2 domain"
/db_xref="CDD:pfam00017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agreement WO 0242457-A 1 30-MAY-2002;
Bristol-Wyers Squibb Co. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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3637...1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1 from Patent W00242457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 TGAGAGATTCTGGGTGTCCTA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGAGAGATTCTGGGTGTCCTA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX452880.1 GI:21712520
                                                                                                                                                                                                                                                                                                                 gene="SLA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                          . 2538
                                                                                                                                                                                                                                                                                                                                                               SLAP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Query Match

Matches

원

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

TITLE

DEFINITION

RESULT 5 AX452880 LOCUS

source

FEATURES

JOURNAL

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repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.; EMBL; Sw.; SMISSPROT; Tr.; TREMBL; Wp.; WORNER; Information on the WORNER database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 20.

Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chhz0

IMPORTANT: This sequence is not the entire insert of clone RP3-460J8 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP3-460J8 is at 66741 in this sequence. The true left end of clone RP3-460J8 is at 100 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequencing problems, such as compressions and repeats, all regions were covered by the quality data (i.e., phred quality >= as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP3-460J8 is from the further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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Src homology 2 (SH2) domain )"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="dJ460J8.2 (novel protein tyrosine kinase with Src homology 2 (SH2) domain )"
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match: ESTS: Em:BG178487"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Continues in Em:AL050318 as dJ977B1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375, 2402
note="14 copies 2 mer ta 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
complement(join(<240, .339,6995, .7085))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(<240. .339,6995. .7128))
/gene="dJ977B1.1"
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//note="match: G8S: Em:AQ556467"

//note="match: G885, .7492)

//note="match: G8S: Em:AQ556478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              783. 3155 "note="match: GSS: Em:AQ807191"
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Thote="match: STS: Em:HS427J1S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: GSS: Em:B45150"
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/gene="dJ977B1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organisma"Homo sapiens"
|mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="q11.21-11.23"
/clone="RP3-460J8"
/clone_lib="RPCI-3"
complement (50. .544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .544)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .66741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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Join (1922. .19451, 22110 .22282, 26087. .26127,30796. .30847)

join (1922. .19451, 22110 .22282, 26087. .26127,30796. .30847)

Anote = march: STS: Em: G23762.

2247. .22282, 26087. .26134,30796. .30847,30986. .31051,

32039. .32142,37091. .37147,46566. 46652,48268. .48328,

50163. .50255,53242. .53362,54429. .>54534)

/mote = movel protein (FLJ13556) similar to N-myc

downstream regulated (NDRG1)
                                                                                                                                                                                                                                                                                                                                                                                               complement(join(<17523. .19451,20551. .20589,22110. .22161,
22247. .22282,26087. .26134,30796. .30847,30986. .31051,
32039. .32142,37091. .37147,46566. .46652,48268. .48328,
50163. .50225,33242. .53362,54429. .>54534)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Em:X22845 Em:AR004162 Em:U60593 Em:AF045564 Em:AB033921
Em:AR159092 Em:AR147402 Em:M59814
match: ESTS: Em:AA718726 Em:AA039000 Em:AW003952 Em:W89263
Em:AA325826 Em:AA718726 Em:AAA162360 Em:AW003952 Em:W89263
Em:AA325935 Em:T85147 Em:AA162360 Em:AA413437 Em:AA104026
Em:T88705 Em:AR386673 Em:AI186615 Em:AAA13437 Em:AI004026
Em:T88705 Em:AV002368 Em:AI181197 Em:AA764653 Em:AA316771
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YFLQGMGYIPYVQLSHLSTESVPSASMTRLARSRTHSTSSSLGSGESPFSRSVTSNQS
DGTQESCESPDVLDRHQTMEVSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'protein_id="CAB65625.1"
'db_xref="vG1:6687781"
'db_xref="vGA:09UGV'
'db_xref="sQA:09UGV'
'db_xref="sWA:SS-PROT:Q9UGV''
'translation="EHDIETTHGVVHVTIRGLPKGNRPVILITYHDIGLNHKSCFNAFF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHFGGEELQANLDLIQTYRMHIAQDINQDNLQLFLNSYNGRRDLEIERPILGGNDNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31GVGAGAYILSRFALNHPELVEGLVLINVDPCAKGWIDWAASKLSGLTTNVVDIILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           match: proteins: Sw:Q62433 Sw:Q92597 Tr:Q9Z2L9 Sw:P97862"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFEDMQEITQHFAVCHVDAPGQQEGAPSFPTGYQYPTMDELAEMLPPVLTHLSLKSI
                                              'note="MER21B repeat: matches 422. .785 of consensus"
                                                                                                  .422 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="match: cDNAs: Em:AB033922 Em:U52073 Em:D87953
                                                                                                                                                                                                     repeat: matches 1. .355 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="dJ460J8.1 (continued from dJ469A13.3 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evidence=not experimental
product="dJ460J8.1 (continued from dJ469Al3.3 in
m:AL132768)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="HY1 repeat: matches 1. .109 of consensus"
                                                                                                                                                      .374 of
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/note="28 copies 2 mer ta 78% conserved"
34564. .34611
                                                                 /note="match: GSS: Em:AZ067993"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ592789"
complement(27980, .28556)
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4313. 34420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                      complement (17522)
complement (17523. .54534)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="dJ469Al3.3"
7555, .17813
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copies 2 mer
                                                                                                                                                                                                     complement (17516)
17519. .1760c
                                                                                                                                                                                                                                                                                                        complement (17521,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="dJ469A13
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                        repeat_region
                                                                                                                           repeat_region
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                                                                                                                                                                                                                              polyA_site
misc_feature
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polyA_site
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11435
11535
14383
14483
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17249
19240
19340
21103
21203
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25883
28825
8925
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34680
34780
                                                                                                             TITLE
JOURNAL
                                                                                                                                                                             COMMENT
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Stren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barria, N., Bastlen, V., Bada, F., Bodukhgalter, B., Brown, A., Burkett, G., Bodukhgalter, B., Brown, A., Burkett, G., Colk, Colk, B., Coke, P., Dearlano, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Rerreira, P., Fitzhugh, W., Gasp, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Rorton, L., Karasan, J., Gardyna, S., Ginde, S., Goyette, M., Rorton, L., Karan, L., Landers, T., Lehoczky, J., Kalin, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Marcdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., Mihova, T., Mihova, T., Minova, T., Minova, T., Minova, T., O'Donnell, P., Wolli, D., Olivar, T.M., Olivar, J., Peterson, K., Petersen, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC026539 145833 bp DNA linear HTG 27-APR-2000 Homo sapiens chromosome 20 clone RP11-712N14 map 20, WORKING DRAFT SEQUENCE, 37 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="TIGGER2 repeat: matches 1780. .2541 of consensus"
60719. .61831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 149.8) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 20; clone RP11-712N14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="TIGGER2 repeat: matches 2541. .2714 of consensus"
59738. .60495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                           .1278 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MERIIC repeat: matches 1. .1071 of consensus"
62547. .63174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 9; Length 66741;
Pred. No. 0.47;
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note="24 copies 2 mer ta 79% conserved"
                                                                                                                         /note="45 copies 2 mer ta 76% conserved"
52922. .53120
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/note="match: GTS: Em:G07504"
complement(57696. .58013)
/note="match: STS: Em:G07632 Em:G07634"
58856. .59001
      42553. 43658
700te="MIRR52C repeat: matches 1.
17989. 48470
                                                                                  /note="match: GSS: Em:AQ672417"
19391. .49480
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match: STS: Em:GS5853"
54054. .54477
                                                                                                                                                                  /note="match: STS: Em:G04621"
complement(53426, .54032)
/gene="dJ469A13.3"
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Homo sapiens (human)
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AUTHORS
TITLE
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AUTHORS
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Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (2-MAR-2000) Whitehead Institute/MIT Center for Genome Submitted (2-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:7283243.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: 17115
Center zone name: 712 N 14
Center clone name: 712 N 14
Center clone name: 712 N 14
Center clone name: 712 N 14
Center clone name: 712 N 14
Contenting vector: M13; M7815; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 125577 bases at least Q40
Consensus quality: 135773 bases at least Q20
Innert size: 182000; agarose-fp
Innert size: 182000; agarose-fp
Innert size: 182000; agarose-fp
Innert size: 142233; sum-off-contigs
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37527:

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clone lib="RPCI-11 Human Male BAC"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/chromosome="20"
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AC005079_1 100001 210000
AC005079_2 200001 310000
AC005079_3 300001 410000
AC005079_4 400001 415268
Continuation (3 of 5) of AC005079 from base 200001 (AC005079 Homo sapiens BAC clone CTA-:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 170128)
Waterston,R.H.
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100.0%; Score 22; DB 2
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 22; Conservative 0; Mismatches
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88.2%; Score 19.4; D

Best Local Similarity 95.2%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches
                         The sequence of Homo sapiens clone Unpublished C [Dases] to 170128)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                              7234. 51023 "note="assembly_fragment" 1124. 54935 "note="assembly_fragment" note="assembly_fragment"
          note="assembly_fragment"
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55036._.59553
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HTG; HTGS PHASE1.
Homo sapiens (human)
Homo sapiens
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AC005079 0
AC005079 1
AC005079 2
AC005079 3
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AC005079 2
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JOURNAL

COMMENT

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ACUUDUSS 224064 bp DNA linear HTG 13-MAR-1999
HOMO Sapiens clone RG050N15, *** SEQUENCING IN PROGRESS ***, 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-JUN-1998) Genome Sequencing Center, Washington Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA.

* NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1.

HTG; HTGS_PHASE1.

Howo sapiens (human)

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gap of unknown 1
contig of 2173 b
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            48353 TGAGAGTTCTGGGTGGCCT 48333
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8218:
8235:
10568:
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JOURNAL
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SOURCE
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                                      St. Louis,
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Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. M 63108, USA.

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1663
1679: gap of unknown length
1826: gap of unknown length
1826: gap of unknown length
1826: gap of unknown length
1820: contig of 1637 bp in length
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1824: contig of 1525 bp in length
1825: contig of 1525 bp in length
1826: gap of unknown length
1827: gap of unknown length
1828: contig of 1225 bp in length
1831: gap of unknown length
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1832: gap of unknown length
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1833: gap of unknown length
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1838: contig of 1329 bp in length
1838: contig of 1329 bp in length
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1833: gap of unknown length
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1834: contig of 6332 bp in length
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1835: gap of unknown length
1836: gap of unknown length
1837: gap of unknown length
1838: contig of 6332 bp in length
1839: contig of 6322 bp in length
1830: contig of 1325 bp in length
1830: contig of 1325 bp in length
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18482: contig of 18673 bp in length
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18484: gap of unknown length
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18485: contig of 18676 bp in length
18486: contig of 18676 bp in length
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95.2%; Pred. No. 16;
cive 0; Mismatches 1;
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Best Local Similarity 95.29
Matches 20; Conservative
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FEATURES

ORIGIN

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GVTKCLLRARRQCKLLIMSATINVELFHGYFGEGARLVQVPGRLFFTKLRYLPPPAL
ELAGQATSKRSQRNIDPAPPVQULELIDQQYPTSRGDVIL FVSGYNEISSYVBAV
HEYATBGTHHUVL PLASGQALADQSKVFDYAABCGMRKCIVSTNIAETSLTVDCWRFVV
DSGKVKEMNFDATCKGQRLKEFWVSKSSADQRKGRAGRTGFGVCFRLYTAAEQYNAFEA
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TSRVVIVAGDTGCGKSTQVPQVLYDFGYRSIACTOPRRLACVSLCKRVAHELLDDVGS
RVAFQIRFERSRTKLTNILFITEGLLLRQLAVAANLDQYDALILDETHERNLFGDFLL
                                                        /strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="18C8-18C8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Longest ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="mRpS14"
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Best Local Similarity 90.9%;
Matches 20; Conservative (
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AC015346/c
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TITLE
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Drosophila melanogaster

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Bukaryota, Descaraca, Diptera, Brachycera; Muscomorpha;

Ephydroidea, Drosophilidae, Drosophila.

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,

Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,

Gonzalaz, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J.,

Nunco, J., Pacleb, J., Parkagas, V., Park, S., Phouanenavong, S., Wan, K.,

Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.

Direct Submission

Burkeley Cabassion

Submitted (08-OCT-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA

Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA

Sequence clones from Trosophila Gene Collection I (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming priming from contaminating genomic DNA, retained introns
due to reverse transcriptuse errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
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196521: gap of unknown length 19625: qap of unknown length 19626: contig of 13287 bp in length 1626 136119: contig of 136487 bp in length 1120 136136: gap of unknown length 157328: contig of 21192 bp in length 157345: gap of unknown length 16995: contig of 21192 bp in length 16995: contig of 21953 bp in length 16933 224064: contig of 21953 bp in length 19833 224064: contig of 25082 bp in length 19833 224064: contig of 25082 bp in length 1966 196321 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of unknown length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 25082 bp in length 196821 gap of 
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Pred. No. 16;
0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RG050N15"
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Location/Qualifiers
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AY058623.1 GI:16198106
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1 Similarity 95.2%;
20; Conservative
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119626
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
AC015346
AC015346.1 GI:6435989
HTG 16.435989
                                                                            PLSKRHQLLCYQSLLETAKPYLINCIRLPAAQTILLESFAIDTNAGITQIACDGWLGL
DLPMPGSGWELLRRAIELRRASRLLYDKLDDLKSKQESPSHSSDDRSSALWQDLVDY
WALDVAYAIRRLLPADIKRLYTHQAPSARLAELKENPFAVDFPWTPNEEKGGLNVSEH
ILESCGMVVASDSDSQLTSAERATRHGELRQLKAMKRRQRFEQPRQRKLLKQSAGRVA
EDEEEQEEAQGDDMRDVDFRLRFDPRQLALLERSSRLDRHSVVVLLKLLLGSGFYPQL
                                                                                                                                                                     VVY SCLAEQQWTTAMDATLRAEPWQCTRCDFELEEFDVLEQLVHRSKCKRRKAQESRT
AKTTSTESSTEVASSSSSHSSGGYYCNSCKRELRLTTIDILRHKKQCRNNK"
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                                                    aisdefnyckgggoffhtrlkpfvlohpnsofakhfellkltesdllpkpdfytpkl
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This sequence was identified as CDM:10210169 by the submitter.
For further information on this sequence.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
1. .26121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Haxapoda; Insecta, Pterygota,
Boyera, Endopteryyota; Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.

1. (bases 1 to 26121)
Adama, M. and Venter, J.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                       DB 3; Length 3521;
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Pred. No. 27;
0; Mismatches
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organism="Drosophila melanogaster"

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AC010847.11 GI:13374650
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2 (bases 1 to 180213)
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Best Local Similarity 90.9°
Matches 20, Conservative
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AC010847/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases 1 to 17917)

Abola, A.P., Bruno, D., Com, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Maco, J., Komp, C., Kottler, S., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-MAR-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Stanford DNA Sequencing and Technology Development
                                                                                                                                                                                                                                                                                                                                                              AC025824 177917 bp DNA linear PRI 19-MAR-
Homo sapiens chromosome 15 clone RP11-430M3, complete sequence.
AC025824
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                                                                                                                                                                       Gaps
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Contact: hum-info@sequence.stanford.edu
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-MAR-2002) Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA On Mar 19, 2002 this sequence version replaced gi:18252013.
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0
                                                                                                                   Length 26121;
                                                                                                                                                                     Indels
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                                                                                                                   th 85.5%; Score 18.8; I Similarity 90.9%; Pred. No. 31; 20; Conservative 0; Mismatches
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Center clone name: RP11-430M3
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                                                                                                                                                                                                                                            5183 TGAAAGAGTTCTGGGTGTCCAA 5162
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1. .177917
                                                                                                                                                                                                            1 TGAGAGTTCTGGGTGTCCTA 22
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                                                                                                                                       Local Similarity
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                                                                                                                   Query Match
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DEFINITION
ACCESSION
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AC025824/c
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AUTHORS
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REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                Matches
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
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                                                                       ORIGIN
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Eukaryotta Metazoa, Atthropoda, Hexapoda, Insecta, Pterygota,
Eukaryotta Metazoa, Atthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
E phydroidea, Drosophila.
E phydroidea, Drosophila.
E celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanaideas, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Besson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K.K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E. Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T. C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Phouanneavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Indun, ishad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence.
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128. .i31
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sequence and target site duplication, CATT, have been removed from completed sequence."
23502. .2380
/note="Single-ttranded, single chemistry with consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster, chromosome X, region 18D-18D, BAC clone
BACR10M08, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 177917;
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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Pred. No. 35;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        quality below 30."
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archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu.
Location/Qualifiers
1. .180213
1. .180213
| Arganism="Drosophila melanogaster"
| And Lype="genomic DNA"
| Strain="Y; on bw sp"
| Ab xref="taxon:7227"
| Abromosome="X"
| Amp="180"="X"
| Amp="180"="X"
| And Argin (D904)"
| Clone="BACRIOMO8 (D904)"
| Clone="BACRIOMO8 (D904)"
| Clone="BACRIOMO8 (D904)"
| Clone="BACRIOMO8 (D904)"
| And Argin (Dosophila melanogaster BAC library, partial EcoRI in pBACe3.6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.9%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 2; Indels 0;
                                                                  FEATURES
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Search completed: February 19, 2004, 23:23:28 Job time: 101.318 secs

8 &

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Abk61507 Human NOV Abk61465 Human CDN Aad43980 Human Src Abc98600 Human ORF Ab 72800 Procochi	AD128808 DIOSOPHILI ADX70675 Human cDN Ad30568 Human pro Ad30568 Human gke Ad303033 PNN AD00000000000000000000000000000000000	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Aca35390 Prokaryot Aca3629 Viral rep Ab102914 brosophil Ada72333 Rice gene Aak73700 Human imm
SUMMARIES ID	ABK61507 ABK61465 AAD43980 ABQ98670 ABC98809	ABL28808 ABX128808 AAD30568 AAH57383 AAS79933	ACHOS682 AAT32455 AAK67913 AAK67913 AAK66372 ACA49310 ACA51118 ACA51177	ACA35390 AAC93029 ABL02914 ADA72333 AAK73700
DB	00.004	41/041	) 00 Cl 4 4 4 L L L L l	- W 4 L 4
* Query Match Length DB	22 1183 2567 763 3319	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	25.00 25.00	1457 13327 340 1382
% Query Match		1867 1867 1867 1867 1867 1867 1867 1867	200888886 2008888886 1114888888	78.2 78.2 76.4 76.4
Score	22 22 22 4.8	80000		17.2
Result No.		0 9 9 9 10 10	000 1111111111111111111111111111111111	0 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Adb62889 Human cDN Ab106558 Drosophil Ab483555 Human cDN Aaf21001 Human pro Ab190153 Human porl Aat64550 Activated Aab66577 Human act Aa520855 Polymucle Aa520855 Polymucle Aa520855 Polymucle Aa520855 Polymucle Aa519829 Drosophil Ab113023 Drosophil Ab113023 Drosophil Ab228780 Human cDN Abc7208 Human pro Abc7208 Human pro Abc7208 Human pro Abc7208 Human pro Abc7208 Human cDN Abc7309 Human cDN Abc7309 Human cDN Abc7309 Human cDN Abc7309 Human cDN Abc7309 Human cDN Abc7309 Human cDN Abc7309 Human cDN Abc7309 Human cDN Abc7309 Human cDN Abc7309 Human CDN Abc7309 Human CDN Abc7309 Human CDN Abc7309 Human CDN Abc7309 Human CDN Abc7309 Human CDN Abc7309 Human CDN Abc7300 Human CDN Ab113022 Drosophil				cardiomyopathy; atherosclerosis; metabolic pathway modulation disorder; a; lymphoma; prostate cancer; primer; graft-versus.host disease; Exon linking; ome; AIDS; asthma; Crohn's disease; defects; multiple sclerosis; inflammation; phy; reverse transcriptase PCR.			M, Kekuda R, Shimkets RA; Topper JN, Yang R;	a disorder associated with osclerosis or cancers. otide (NOVX) a mature form of than 15%), the nucleotide
2394 9 ADB62889 5313 4 ABL06558 701 4 AAF23001 1191 6 ABL90353 11273 2 AAF64550 11621 2 AAC5456 1621 4 AAS59292 1621 4 AAS59292 1621 4 ABL13023 2872 4 ABL13023 2872 4 ABL13023 2872 4 ABL13023 2872 4 ABL13023 2872 4 ABL13023 2872 4 ABL13023 2872 4 ABL13023 3986 5 ABV2878 4665 6 ABK83947 5912 4 ABL19828 7420 4 ABL13022	ALIGNMENTS	DNA; 22 BP.	. entry) primer #2.	ne therapy; ing disorder denocarcinom ne response; ciency syndr ciency syndr oital heart osteodystro		-USO26510. -0228191P. -0267300P. -026961P. -0277337P.	CS INC. , Grosse WM, Hart S, Tomlinson JE,	or treating or preventing a di. 9. cardiomyopathy, atheroscle. 4; 263pp; English. tes to an isolated polypeptide nt (differing by no more than:
25		T 1 507 ABK61507 standard; ABK61507;	18-JUN-2002 (first Human NOV13 RT-PCR )	ss; NOVX; gignal proceses; cancer; cancer; two cancer; two cancer; the cancer that the cancer conston; constant cancer ca	MO200216599-A2.	27-AUG-2001; 2001WO- 25-AUG-2000; 2000US- 08-FEB-2001; 2001US- 20-FEB-2001; 2001US- 20-MAR-2001; 2001US-	(CURA-) CURAGEN CORP. (CORT-) COR THERABEUTI Burgess CE, Conley PB Spytek KA, Szekeres E WPI; 2002-280937/32.	polypeptides f n, in humans, e nple 2; Page 23 invention rela K, a NOVX varia
		RESUL ABK61 ID XX AC	EXEX	**************************************	8	* * * * * * * * *	XX P P I XX D XX D XX D XX	X

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cc encoding NOVX (or its complement, fragment or variant). NOVX is NOV1-14, Cc 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic acid encoding it can and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NOVX-associated disorder in humans, e.g. cardiomyopathy, atheres or cancers. The NOVX polypeptide contained are also useful for determining the presence of predisposition to the diseases. The NOVX nucleic acid and polypeptide are predisposition to the diseases. The NOVX nucleic acid and polypeptide are concers described with aberrant NOVX expression or activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer uterus cancers (immune response, graft-versus-host disease, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension, congenital heart defects, multiple soleroais, inflammation or Albright hereditary osteodystrophy and many other diseases listed in the conditions. The DNA encoding the protein is useful in gene therapy for treating the conditions. This is also useful in detection assays, or concern the DNA encoding the protein is useful analysis of various for developing a powerful assay system for functional malysis of various human disorders, as well as in diagnostic applications. The present consequence is a reverse transcriptase (RT)-PCR primer used to measure consequence is a reverse transcriptase (RT)-PCR primer used to measure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; limine response; graft-versus-host disease; acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; cell signal processing disorder; metabolic pathway modulation disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 22; DB 6; Length 22; 100.0%; Pred. No. 0.79; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22 BP; 4 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGAGAGAGTTCTGGGTGTCCTA 22
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Albright hereditary osteodystrophy
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(CORT-) COR THERAPEUTICS INC.
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08-FEB-2001; 2001US-0267300P.
06-FEB-2001; 2001US-026961P.
20-MAR-2001; 2001US-026961P.
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Szekeres ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 22; Conservative
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P-PSDB; AAU91308.
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The invention relates to an isolated polypeptide (NoVX) a mature form of NOVX, aziant (differing by no more than 15%), the nucleotide concoding NOVX (art its complement, fragment or variant). NOVX is NOV1-14, 15a, 15b, 16a, and 16b. The NOVX plypeptide, nucleic acid encoding it and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NOVX-associated disorder in humans, e.g. cardiomyopathy, atherosclerosis, a disorder related to cell signal processing and metabolic pathway meduation, diabetes or cancers. The NOVX polypeptide metabolic pathway meduation, diabetes or cancers. The NOVX polypeptide are predisposition to the diseases. The NOVX nucleic acid and polypeptide are predisposition to the diseases. The NOVX nucleic acid and polypeptide are specially useful in therapeutic or prophylactic applications for disorders associated with aberrant NOVX expression or activity, e.g. cancers) immune response, graft-versus-host disease, hypertension, cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus cancers) immune response, graft-versus-host disease, hypertension, companital heart defects, multiple scherosis, inflammation or Albright hereditary osteodystrophy and many other diseases listed in the specification. The DNA encoding the protein is useful in gene therapy for treating the conditions. This is also useful in detection assays, or property and analysis or treating the conditions that is also useful in the conditions that is also useful in the conditions that is also useful and assays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome mapping, tissue typing, diagnostic or prognostic assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present sequence encodes a NOVX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, SH2/SH3-domain-containing adapter; Src-Like Adapter Protein-2; SLSAP-2; immune disease; cancer; Sh2P-2; immune disease; cancer; neoplasm; inflammation disorder; rheumatoid arthritis; osteoarthritis; psoriasis; rhinitis; allergy; inflammatory bowel disease; gene therapy; Crohn's disease; systemic lupus erythematosus; tissus/organ rejection; multiple sclerosis; asthma; acute respiratory distress syndrome; pulmonary disorder; dermatological; neuroprotective; gene; sex
                    New polypeptides for treating or preventing a disorder associated with them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                            Claim 1; Page 98; 263pp; English
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nes 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2001; 2001WO-US043367
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Matches
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Kanner SB;

Perez-Villar JJ,

Whitney GS,

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The invention relates to a substantially purified human SH2/SH3-domain-
C containing adapter polypeptide, termed Src-Like Adapter Protein-2 (SLAP-
CC 2). The invention is useful for treating an immune disorder involving
CND the invention is useful for treating an immune disorder involving
CND MSLAP-2 with cellular signalling compounds, for diagnosing, treating or
CC SIAP-2 with cellular signalling compounds, for diagnosing, treating or
CC STAP-2 with cellular signalling compounds, for diagnosing, treating or
CC STAP-2 with associate with hSLAP-2 and which provide critical signals
CC cellular signal transduction, for determining those cellular signalling
CC cellular signal transduction, for determining those cellular signalling
CC condition. The invention is useful in screening assays to identity and
CC activation. The invention is useful in screening assays to identity and
CC activation. The invention is useful in screening assays to identity for
CC conditions to treat autoimmune diseases which may be caused
CC potential use to treat autoimmune diseases which may be caused
CC potential use to treat autoimmune diseases which may be caused
CC potential use to reat autoimmune diseases which may be caused
CC potential use to real autoimmune diseases which may be caused
CC potential use colls, in addition to other immune system related
CC conditions, diseases, or discorders, T-cell and S-cell neoplasms,
CC and ulcerative colities, althinities, inflammatory bowel disease (crhn's
CC mast cells or eosinophils, autoimmune diseases such as systemic lupus
CC mast cells or eosinophils, autoimmune diseases such as systemic lupus
CC mast cells and T-cells, or other immune cells, such as
CC mast respiratory distress syndrome, and chronic obstructive
CC pulmonary disorder, tissue/ organ rejection and cancer. The invention is
CC useful in gene therapy. The present sequence is human SLAP-2 cDNA
                                                                                                                                                                                                                             Novel substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-Like Adapter Protein-2, useful for therapeutic intervention in immunological and inflammatory disorders and cancer.
                           (BRIM ) BRISTOL-MYERS SQUIBE CO
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                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 1; 85pp; English.
                                                                                     Chang H, Yang W, Wu Y,
                                                                                                                                          WPI; 2002-463632/49.
P-PSDB; AAE26357.
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ABQ98670
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Gaps 0 100.0%; Score 22; DB 6; Length 2567; 100.0%; Pred. No. 1.3; Sequence 2567 BP; 611 A; 741 C; 666 G; 549 T; 0 U; 0 Other; 0; Indels Mismatches ö Query Match
Best Local Similarity 100.
Matches 22; Conservative

22 1 TGAGAGAGITCTGGGTGTCCTA

04-NOV-2002

US2002082206-A1

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241 főAGAGAGTÍCTGGGTGTCCTA 262

ABQ98670; 

(first entry)

Human ORF477 coding sequence.

Cytostatic, Cardiant, Anti-allergic, Immunosuppressive, Vulnerary, Antiniflammatory; gene therapy; human; ORFX; atherogenic; platelet; human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy, autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder; ds.

27-JUN-2002

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The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631-ABP64681 and ABQ99194-ABQ99267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                           New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
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                                                                                                                                                                             Law
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                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 953; 78pp; English.
                                                                                                                                                                        Conley PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGAGAGAGTTCTGGGTGTCCTA 22
 30-MAY-2001; 2001US-00867550
                                     30-MAY-2000, 2000US-0208427P
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Best Local Similarity 95.5'
Matches 21, Conservative
                                                                                                                                                                          Mehraban F,
                                                                LEACH M D.
MEHRABAN F.
CONLEY P B.
TOPPER J N.
LAW D.
                                                                                                                                                                                                         WPI; 2002-626554/67.
P-PSDB; ABP64107.
                                                                                                                                                                          Leach MD,
                                                                                                   (CONL/)
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Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster genomic polynucleotide SEQ ID NO 37900. 112 readadadricideargrecta 133 ABL28809 standard; DNA; 3319 BP. 26-MAR-2002 (first entry) pharmaceutical; gene; ds Drosophila melanogaster ABL28809; RESULT 5 ABL28809 

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23-MAR-2001; 2001WO-US009231. 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. 27-SEP-2001.

WO200171042-A2.

(PEKE ) PE CORP NY

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Gaps

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Indels

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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene; NOVX; metabolic disorder; diabetes; cardiomyopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obesity, infectious disease, anorexia, neurodegenerative disorder, Albahamer's disease, Parkhinson's disease, immune disorder; haematopoietic disorder; dyshipidaemia, metabolic disturbance; metabolic syndrome X; wasting disorder; cancer; gene therapy; SNP;
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/standard_name= "Single nucleotide polymorphism"
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                                                                                                                 Sequence 5782 BP; 1326 A; 1604 C; 1561 G; 1291 T; 0 U; 0 Other
                                                                                                                                                     DB 4; Length 5782;
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Pred. No. 48;
0; Mismatches
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replace(78,C)
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2001US-0286548P.
2001US-02917659.
2001US-0311595P.
2001US-0318980P.
2001US-0318526P.
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2001US-0276400P.
2001US-0276677P.
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Best Local Similarity 90.9%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA encoding NOV26.
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16-MAR-2001;
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                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABIL16176-ABIL0611), expressed DNA sequences (ABIL16175) and the encoded proteins (ABBS7137-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
                                                                      isolated nucleic acid detection reagent for detecting 1000 or more as from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genomic polynucleotide SEQ ID NO 37897.
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 3319;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3319 BP; 699 A; 947 C; 992 G; 681 T; 0 U; 0 Other;
                                                                                                                                                 Claim 1; SEQ ID NO 37900; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 37897; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.8;
Pred. No. 45
EW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1729 reaaaaaarrereegrereeaa 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGAGAGAGTTCTGGGTGTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                       85.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL28808 standard; DNA; 5782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-0191637P, 11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 90.9 es 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
Adams M,
                                  WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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RESULT 6
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Matches

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10-SEP-2001;

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The invention relates to an isolated polypeptide termed NOVX (NOV1, 2a, 2b, 3a, 3b, 4a, 4b, 5, 6, 7a-c, 8a-e, 9a-b, 10, 11, 12a-c, 13, 14, 15, 2ca-b, 20a-b, 21-30) appearing as ABUS528-4, a variant of NOVX, a mature form of NOVX, and a variant of the mature form of NOVX, and a variant of the mature form of NOVX, and a variant of the mature form of NOVX and a vector comprising NOVX (NOVX). A second of comprising the vector, an anti-NOVX antibody (ab), determining the presence or amount of NOVX or NOVX NA in a sample, and identifying an agent that binds or modulates the expression or activity of NOVX. NOVX, NOVX, NOVX, NOVX, NOVX NA or ab is useful for treating or preventing a NOVX-associated disorder in a subject, preferably human. Ab is useful for identifying an agent that binds or modulates the expression or activity of NOVX. NOVX, NOVX NA or ab is useful for treating or preventing a NOVX-associated disorders, and agent that binds or mount of NOVX in a sample. NOVX is useful for treating or preventing a NOVX associated disease, anorexia, neurodegenerative disorders, Alzheimer's disease, contact of a sorders, Alzheimer's disease, and the metabolic disorders, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic disease, various cancers, endocrine, connective tissue, blood, vascular, protocoal or viral infections. NOVX NOVX NoVX No or ab is useful in screening assays, detection assays, predictive medicine, and in methods of creatment. NOVX is useful assay. NOVX is useful assay. NOVX No or ab is useful in a NOVX cereen for potential antiqual activity. The cell is useful for producing non-human transgenic antimals. The value of a linical testing procedure. The present connective antique and the modulate part of a clinical testing procedure. The present connective encodes a NOVX NoVX and colinical testing procedure. The present
                                                                                                                                                                                                                                                                                                                     New isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
                                                                                                                        EA, Shimkete RA, Li L, Shenoy SG, Kekuda R, Spytek KA; CAM, Malyazikar UL, Guo X, Gueev VY, Gasman SJ, Boldog K, Tchernev VT, Patturajan M, Gangolli EA, Padigaru M, rtner JC, Gerlach VL, Spaderna SK, Zerhueen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 210-211; 479pp; English.
17-SEP-2001; 2001US-0322712P,
18-OCT-2001; 2001US-0330307P,
                                                                                                                     Shimkets RA, L.,
Malyankar UL,
                                                                        (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                     2003-046859/04.
                                                                                                                                                                                                                                                WPI; 2003-046859/
P-PSDB; ABU52620.
                                                                                                                                                                                                  Baumgartner JC,
                                                                                                                                                Vernet CAM
Furtak K,
                                                                                                                          CEA,
                                                                                                                                                                                                                                                                                                                                                                                                        cancer,
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Sequence 2442 BP; 645 A; 631 C; 643 G; 523 T; 0 U; 0 Other;

sequence encodes a NOVX protein

Gaps , 0 79.1%; Score 17.4; DB 7; Length 2442; 94.7%; Pred. No. 2e+02; 1. Indels 0 Mismatches 1; Indels 0 Local Similarity 94.7 nes 18; Conservative Query Match Matches

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AAD30568 standard; cDNA; 2789 RESULT 8

21-MAY-2002

AAD30568;

Human protease, PRTS-1 cDNA.

Human; protease; PRTS-1; enzyme; gastritis; cirrhosis; Crohn's disease;

Gaps

ö

79.1%; Score 17.4; DB 6; Length 2789; 94.7%; Pred. No. 2.1e+02; tive 0; Mismatches 1; Indels 0

Query Match
Best Local Similarity 94.7
Matches 18; Conservative

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PRTS protein and DNA are useful for diagnosing, treating and preventing gastrointestinal disorders (gastritis, cirrhosis, Crohn's disease).

Countinisatinal disorders (gastritis, cirrhosis, Crohn's disease).

Countinisation, cardiovascular disorder (atherosclerosis, hypertension, myocardial infarction), cell proliferative disorders (hepatitis, cancer, psortasis), developmental disorders (Cubling's syndrome, hypothyroidism), epithelial disorder (vitiligo, keloid, eczema), neurological disorders (epitepsy, Alzheimer's disease, Pick's disease, Huttington's disease, Pick's disease, Huttington's disease, cortein is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PRTS DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, or tissues from patients to detect altered PKIN expression. The present sequence is human PRTS-1 cDNA
gastrointestinal disorder; autoimmune; inflammatory; cell proliferative; cardiovascular; developmental; epithelial; neurological; reproductive; AlDS; Acquired Immune Deficiency Syndrome; allorgy; rheumatoid arthritis; anaemia; asthma; atheroscierosis; hypertension; myocardial infarction; hepartitis; cancer; psoriasis; Cushing's syndrome; hypothyroidism; eczema; epilepsy; Alzheimer's disease; Huntington's disease; Parkinson's disease; Pick's disease; infertility; vitiligo; drug screening; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human protease polypeptide, useful in diagnosis, prevention and treatment of gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial and neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Todd S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated human protease polypeptide (PRTS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delegeane AM, Gandhi AR, Hafalia AJA, Lu DAM, Patterson C;
Tribouley CM, Das D; Kallick DA, Nguyen DB, Lee EA, Khan FA,
Au-Young J, Griffin JA, Policky JL, Ramkunar J, Yang J;
Thangavelu K, Ding L, Kearney L, Baughn MR, Borowsky ML;
Sanjanwala MS, Yao MG, Burford N, Walla NK, Lal P, Lee S, Toc
Lo TP, Tang YT, Elliott VS, Azimzai Y, Lu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2789 BP; 715 A; 745 C; 698 G; 631 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            303. .347

*tag= b

48. .2603

*tag= c

/*tag= c

/product= "Mature PRTS-1 protein"
                                                                                                                                                                                                                                                              "Human PRTS-1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 164-165; 182pp; English.
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000US-0220063P.
28-JUL-2000; 2000US-0221680P.
04-AUG-2000; 2000US-022544P.
11-AUG-2000; 2000US-0225989P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-2001; 2001WO-US022397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0227568P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                     303. .2606
/*tag= a
/product= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-206082/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Au-Young J, Griffi
Thangavelu K, Ding
Sanjanwala MS, Yao
Lo TP, Tang YT, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAE19164,
                                                                                                                                                                                                                                                                                                                                                                                                     WO200208396-A2
                                                                                                                                                                Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-AUG-2000;
                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                         mat_peptide
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.

10-MAR-2001; 2001WO-US008631.

WO200175067-A2

11-OCT-2001.

Homo sapiens

31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167

DNA encoding novel human diagnostic protein #26737.

(first entry)

13-FEB-2002

AAS90933;

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AAH57161 to AAH57576 represent cell and tissue specific polymucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhamiticrs, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The developments and for investigating a predisposition to a disorder where the treatments and for investigating a predisposition to a disorder where the gene profile with a cancer, immunopathology or neuropathology
                                                                                                                                                                                             Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology,
                                                                                                                                                                      Human skeletal muscle cell specific cDNA sequence SEQ ID NO:223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3076 BP; 800 A; 814 C; 792 G; 670 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sornasse T, Seilhamer JJ, Watson GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 153-154; 327pp; English
                    GAGAGTTCTGGATGTCCTA 1360
                                                                                           AAH57383 standard; cDNA; 3076 BP
        22
        GAGAGTICTGGGTGTCCTA
                                                                                                                                                                                                                                                                                                                                         02-NOV-2000; 2000WO-US030396.
                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-291057/30.
                                                                                                                                                                                                                                                                                      WO200132927-A2
                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                              10-SEP-2001
                                                                                                                                                                                                                                                                                                                10-MAY-2001.
                               1342
                                                                                                                      AAH57383;
                                                                             RESULT
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

Ormanac RT, Liu C, WPI; 2001-639362/73.

P-PSDB; ABG26746

(HYSE-) HYSEQ INC

Claim 1; SEQ ID NO 26737; 103pp; English.

biodiversity.

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed centivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in sisue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic dissorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amine acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1784 GAGAGÍTICIGGATGÍCCTA 1802
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Gaps

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1; Indels

0; Mismatches

1244 GAGAGTICTGGATGTCCTA 1262

RESULT 10 AAS90933 ID AAS90933 standard; cDNA; 3210

4 GAGAGITCIGGGIGICCIA 22

Score 17.4; DB 4; Length 3076; Pred. No. 2.1e+02;

79.18;

Local Similarity 94.7 es 18; Conservative

Query Match

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17-JAN-2001; 2001WO-US001354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGMD2 disease
                                                                                                                                                                                                                                                 21-NOV-1995;
                                                                                                                                                    polyA_signal
                                                                                                                                                                                            WO9616175-A2
                                                                                                                                                                                                                                                                            22-NOV-1994;
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                            CAAT_signal
                                                                   TATA_signal
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#XBXBXSXMXXBXBXXXXXB
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                                                             Gene therapy, emphysema; ss; gene; chronic obstructive pulmonary disease; respiratory disorder; lung cancer; asthma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a combination comprising cDNAs or their complements that are differentially expressed in respiratory disorder. The combination is useful for preparing a composition for diagnosing or treating respiratory disorders e.g. lung cancer, chronic obstructive pulmonary disease, emphysema or asthma. The present sequence represents human cDNA differentially expressed during lung cancer
                                                                                                                                                                                                                                                                                                                              New combination comprising cDNAs that are differentially expressed in respiratory disorders, useful for diagnosing or treating respiratory disorders e.g., lung cancer, chronic obstructive pulmonary disease, emphysema or asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                   Human cDNA differentially expressed in lung cancer #87
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759. .764
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/label= Alu sequence.
712. .716
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109. .359
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                                                                                                                                                                                        04-APR-2002; 2002US-00116802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.1%;
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page; 39pp; English
                                                                                                                                                                                                                    04-APR-2001; 2001US-0281593P
          26-SEP-2003 (first entry)
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Best Local Similarity 94.7
Matches 18, Conservative
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                                                                                                                                 US2003065157-A1
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misc_feature
                                                                                                       Homo sapiens
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Human novel Calpain large sub:unit 1 gene encoding a calcium dependent protease - used to develop prods. for the diagnosis and treatment of limb-girdle muscular dystrophy 2 disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The calpain large subunit 1 gene located on chromosome 15 codes for a calcium activated neutral protease (CANP3) belonging to the calpain family. Mutations in the gene induce limp-girdle muscular dystrophy (LGMD) 2 disease. The gene, and fragments of it, can be used in the prevention, treatment, diagnosis and detection of a predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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cytostatic, gene therapy, vaccine, metastasis, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5149 BP; 1343 A; 1312 C; 1179 G; 1314 T; 0 U; 1 Other;
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/4288. 4293
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270. .1275
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note= "Putative TATA signal.
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PR 20-0CT-2000; 2000US-02492P.
PR 20-0CT-2000; 2000US-02492P.
PR 20-0CT-2000; 2000US

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
transmit of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
pupplement the patients own production of (I). Additionally, (I)
polymucleotides may be used to produce the secreted (I), by inserting the
protein. (I) proteins and polymucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
to AAK87694 represent human immune/haematopoietic artigen genomic
sequences from the present invention. AAK45492 to AAK87693 and AAM82169
represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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Disclosure; SEQ ID NO 22725; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
78.2%; Score 17.2; DB 4; Length 355;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels
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Sequence 356 BP; 121 A; 76 C; 74 G; 85 T; 0 U; 0 Other;

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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 22724; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polyuucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the protein. (1) proteins and polynucleotides may be used to protein each of a cancer metastases of haematopoietic-derived cells AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64942 to AAK87699 and AAM82169 represent sequences used in the exemplification of the present invention

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                                                                                                                                                    Human, immune, haematopoietic, immune/haematopoietic antigen, cancer, cytostatic, gene therapy, vaccine, metastasis, ss.
                  Gaps
                                                                                                                                    Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:1432.
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 Length 356;
Query Match

78.2%; Score 17.2; DB 4;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3;
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                                22
                                                                                     AAK56372 standard; cDNA; 359 BP
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16-MAR-2000;
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19-MAY-2000;
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28-JUN-2000;
30-JUN-2000;
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11-JUL-2000;
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PR 18-DEC-2000; 200US-035318P,
PR 18
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Gaps

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Query Match
78.2%; Score 17.2; DB 4; Length 359;
Best Local Similarity 86.4%; Pred. No. 2.18+02;
Matches 19; Conservative 0; Mismatches 3; Indels

Search completed: February 19, 2004, 21:51:47 Job time : 24.3821 secs

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February 19, 2004, 21:21:54 , Search time 145.664 Seconds (without alignments) 4510.152 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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BX383606 BG178487 BQ053486 BQ054265

2222

616 778 878 986

100.0 100.0 100.0

22222

	AV572518 RPCI-74-7 CA955326 CCLL010404 CC2505491 CT261-127 BX500783 DKFZp779B BX500783 DKFZp779B B1430374 £490603.Y AA12424-7 AA1249071 RPCI-44-7 CE51267 £195994 AA749071 RPCI-24-7 CE51267 £1976 BU065505 F9r CE51267 £1976 CE51319 AGENCOURT AL411370 T3 end of AX413977 H9mc sapi AA64082 DKZ4b06.T BB700751 BB730751 BR70751 BB730751 BR75867 BY675867 CG578968 OST216823 AV797883 AV797883 BE64580 UI-M-AII- BE846016 UW31911.X	AA699188 vr62e01. AA69188 vr62e01. AZ64203 RPCI-2201. AZ264203 RPCI-2201. LINE) COT 10-NORMALIZ 5-PRIME, mRNA sequence. a; Vertebrata; Euteleostominin; Hominidae; Homo. Lization ncage www.genoscope.cns.fr cologies, a division of sequence cluster 9825.r For see		
BQ054 ALC322 AZ822 AZ822 AZ822 AZ822 AZ822 BX038 BHB34 BHB34 BHB34 BHB34 BHB34 BHB34 BHB34	AV846834 AV727518 CA565326 CC2500491 CC2500491 BX500783 BX500783 AV598294 AA128423 AV598294 AX598294 CC5511819 CNS06Q2K	ALIGNMEN ALIGNMEN ALIGNMEN 616 bp T CELLS (U ne CSODJ013 52 Esse, U. an aries and n aries and a aries aries and a aries aries and a aries aries aries and a aries aries 1000.0 1000.0 1000.0 1201 1201 1201 1201	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	78.2 439 78.2 440 78.2 440 78.2 440 383606 Homo sap mo sapiens cDNA 383606.1 GI:30 T. T. T. T. T. T. T. T. T. T. T. T. T.
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/tab_host="DH108 (plage-resistant)"
/clone lib="NHH MGC 91"
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Note: this is a NIH_MGC Library."
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                                                                             /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. cow: i column: 01
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Faraday Avenue Genoscope sequence ID : CS0DJ013BF05QP1.
Location/Qualifiers
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100.0%; Score 22; DB 12; Length 778;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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/db_xref="taxon:9606"
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BG178487
                   FEATURES
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/organism="Homo sapiens"
//organism="mRNA"
//db_rref="mRNA"
//db_rref="mRNA"
//db_rref="latural killer cells, cell line"
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//issue of corgan: blood; Vector: poTB7; Site_1: XhoI; Site_2:
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//issue programmed by oligo-dT priming, Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
//issue corganical material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material material materia
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AGENCOURT 6822017 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935253
5', mRNA sequence.
BQ053486.1 GI:19812826
EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: He I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCNZ122 row: 1 column: 06
High quality sequence stop: 394.
Location/Qualifiers
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1 (bases 1 to 878)

NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Gaps

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us-09-939-853a-142.rst

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On reb 15, 2001 this sequence version replaced gi:12871733.

Contact: Genoscope Genoscope - Centra National de Sequencage

BP 191 91006 BYRY cedex - France

Email: seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9825.r For

more information about this cluster, see

http://www.genoscope.cns.fr.

cgi:bin/cluster.cgi?seq-CSODE005AF12QP1&cluster=9825.r. Contact:

Feng Liang Email: fliang@lifetech.com URL:

http://fullleagth.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CSODE005AF12QP1.
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/clone lib="Homo sapiens PLACENTA"

/clone lib="Wedtor: PCMVSPORT 6; lst strand cDNA was primed

with a Not1-oligo(dT) primer. Five prime end enriched,

with a Not1-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

the Not I and ECRV sites of the pCMVSPORT 6 vector.

Library was not normalized."
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1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDRA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 22; DB 12; Length 1020; 100.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 22; DB 9; Length 1201; 100.0%; Pred. No. 36; cive 0; Mismatches 0; Indels C
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/db_xref="taxon:9606"
/clone="CS0DE005YK23"
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AL541041.2 GI:30544829
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                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Irisaue Procurement: Dr. Daniel McVicar, DBS/NCI

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM2125 row: i column: 12

High quality sequence stop: 515.
      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/wol_type="mRNA"
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BQ054281.1 GI:19813621
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gol electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil 473214 | gb | AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptores complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Gossypium hirsutum
Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

1 (bases 1 to 651)
Blewitt,M., Matz,B.C., Davy,D.F. and Burr,B.
ESTS from developing cotton fiber
Unpublished (1999)
Contact: Ben Burr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-", clone lib="Mouse 10kb plasmid UVGCNM library"
/note="Vector: PWD4ZLN; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 83.6%; Score 18.4; DB 28; Length 598; I Similarity 95.0%; Pred. No. 1.1e+03; 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                             Mm. 308, Blomca...
Rm. 308, Blomca...
84112, USA
Tel: 801 585 506
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0.013 row: B column: 18
Seq primer: CACACAGGAACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 598.
Location/Qualifiers
Location/Qualifiers
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plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC2M0103B18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male"
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AI727541
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                                                                                                                                573 bp DNA linear GSS 14-NAY-2003 TAM32-33G24 Sp6.1 TAM32 Gallus gallus genomic clone TAM32-33G24, GC332697
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2M0103B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0103B18 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                              Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Bhasianinae; Gallus.
I (bases I to 573)
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="UCD001, inbred 256"
/clone_lib="TAM32"
/note="Vector: pECBAC1, Site_1: EcoR1; Site_2: EcoR1;
TAM32 Female Chicken library - for library and clone ordering information: http://www.hbz.tamu.edu"
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Pred. No. 7.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Bmail: submissions@wateon.wustl.edu
Insert Length: 152000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/mol_type="genomic_DNA"
/drain="Red_Jungle_Fowl"
/db_xef="taxon:9031"
/dlone="TAX32-33G24"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gallus gallus"
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High quality sequence stop: 478.
Location/Qualifiers
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             TGAGAGAGTTCTGGGTGTCCTA 22
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GSS.
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90.9%;
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Best Local Similarity 90.9
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                                                                                                             RESULT 7
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ORIGIN

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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.

AL Nature 420, 563-573 (2002)

CE (bases I to 2919)

RS Adachi J., Alzawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Harbida, T., Hayatsu, N., Hirancho, K., Harada, T., Hiraokan, T., Horzane, T., Hori, F., Imorani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Itoh, M., Wagazaki, R., Ouno, H., Nawata, M., Nakani, M., Nakani, M., Nakani, M., Nakani, M., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, Y., Sakai, Y., Sakai, Y., Sakai, Y., Sakai, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Hurameru, M., Muzameru, M., And Hayashizaki, Y., Toya, T., Yasunishi, A.,
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2M0199D23R Mouse 10kb plasmid UUGCZM library Mus musculus genomic clone UUGCZM0199D23 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9212,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="RIKEN full-length enriched mouse cDNA library"
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/db_xref="WG1:2399272"
/db_xref="taxon:10090"
/clone="9430080120"
/tissue_type="embryonic body between diaphragm region and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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URL:http://fantom.gec.riken.go.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="12 days embryo"
1. .2919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
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Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK035058 and the many many linear HTC 18-SEP-2003 Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430080120 product:hypothetical protein, full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itob, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                    /organism="Gossypium hirsutum"
/mol_type="mRNA"
/culfiva="Acala Maxxa"
/db_xref="taxon:3615"
/tissue_type="immature fiber"
/dev_stage="Six_days post anthesis"
/lab_host="XII-Blue"
/lone_ilb="Six-day Cotton fiber"
/note="Vector: pBluescript II KS+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.4; DB 9;
Pred. No. 1.2e+03;
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High-effictency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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1 Similarity 95.0%; Pred. No. 1.2e
19; Conservative 0; Mismatches
                            Laboratory
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                    Brookhaven National Laborat
Upton, NY 11973, USA
1281: 516-344-3396
Fax: 516-344-3407
Email: burr@bnluxi.bnl.gov
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Mus musculus (house mouse)
Mus musculus
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Biology Department
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Sequencing
The British Columbia Cancer Agency Genome Science Centre
500 W. 10th Ave. Vancouver, British Columbia, Canada V52 4E6
500 W. 10th Ave. Vancouver, British Columbia, Canada V52 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@becgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the international Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
Plate: 358 row: G column: 5
Seg primer: T7
Class: BAC ends.
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BACPP7-C12.z Pristionchus pacificus BAC ends Pristionchus pacificus genomic, genomic, genomic, genomic,
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                     Bovidae; Bovinae; Bos.

1 (Dases 1 to 296)
Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,
Butterfield, Y., Marson, A., Brown-John, M., Jones, S.,
Scheln, J., Marram, de Jong, P., McWilliam, S., Barris, W.,
Dalrymple, B.D. and Tellam, R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male" | /cell_type="Blood" | /cell_type="Blood" | /cell_type="Blood" | /cell_type="Blood" | /cell_type="Belood: praction | /cell_type="Vector: praction | /cell_type="Vector: praction | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_type="Vector | /cell_t
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Eukaryota, Metazca, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
1 (Dases 1 to 464)
Srinivasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R.,
Srinivasan, J., Mitte, H., Keller, H., Kipping, I., Pires da Silva, A.,
Jesse, T., Milare, J., de Both, M., Schuster, S.C. and Sommer, R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
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80.9%; Score 17.8; DB 29;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
Other GSSs: CH240 358G5.TARBAC13P2
Contact: Rob Holt
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/strain="breed: Hereford"
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/clone="CH240_358G5"
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1. .296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.orgyresources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4712114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 283)
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Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                             Dunn, D. Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralma, L., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Stally, M., Rose, M., Rose, M., Stally, M., Brand, D., Weiss, R., Stokes, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
R. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0199 row: D column: 23
Seg primer: CACACAGGAAACAGCTAATGACC
Class: plasmid ends
High quality sequence stop: 283.
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/mol_type="genomic DNA"
/strain="C57BL/64"
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/clone="UUGC2M0199D23"
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84112, USA
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Length 296; Indels us-09-939-853a-142.rst

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CE606764.1 GI:37167411
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Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, Vitaceae, Vitis.
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/mol type="mRNA"
/mol type="mRNA"
/cultiva="Plnot noir"
/db_txte="taxon:29760"
/sex="Hermaphrodite"
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/lab_host="DH108"
/clone lib="Grape Bud pSPORT1 Library"
/note="Organ: bud, Vector: pSPORT1; Site_1: Not1; Site_2: Sali"
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Moser, C., Segala, C., Fontana, P., Salakhudtinov, I., Gatto, P.,
Pindo, M., Zyprian, B., Toepfer, R., Grando, M.S. and Velasco, R.
Expressed sequence tags from different organs of Vitis vinifera
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: claudio.moser@ismaa.it
The sequencing work has been funded by the 'Fondazione Cassa di
Risparmio di Trento e Roverseto'
High quality sequence stop: 498.

Location/Qualifiers
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Laboratorio di Genetica Molecolare
Estituto Agrario di San Michele all'Adige (IASMA)
via E. Mach 1, San Michele all'Adige (TN), I-38010, Italia
Tel: 0039-0461-615314
Fax: 0039-0461-650956
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1. .464
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="var. California"
/db_xref="taxon:54126"
/clone_lib="Pristionchus pacificus BAC ends"
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               Evolutionary Biology
Max-Pandk-Institute for Developmental Biology
Max-Pandk-Institute for Developmental
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                  80.9%; Score 17.8; DB 28; 90.5%; Pred. No. 1.9e+03; live 0; Mismatches 2;
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Matches 19; Conservative
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GSS 20-MAY-2002
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                                                                                                                                                                                          Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 601)
Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Kaller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
BH826297
BACPP23-008.z Pristionchus pacificus BAC ends Pristionchus
pacificus genomic, genomic survey sequence.
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Max-Panck-Institute for Developmental Biology
Faricology (197071601371)
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

80.9%; Score 17.8; DB 28;
Best Local Similarity 90.5%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 2;
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Job time : 149.664 secs
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                                                                                                                                                                  Pristionchus pacificus
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
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Query Match 78.2%; Score 17.2; I
Best Local Similarity 86.4%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches
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                                     TYPE: DNA
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6747, Ap
11814, A
11984, A
12361, A
                                                                                                      February 19, 2004, 21:32:00 ; Search time 3.56994 Seconds (without alignments) 3419.919 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-313-294A-4815
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US-09-313-294A-2911
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US-09-621-976-788
US-08-916-901-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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US-08-123-161A-9
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US-08-691-563C-52
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US-08-630-915A-193
US-09-595-684B-24
US-09-409-604-1
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Sequence 3698, Application US/09489039A
Patent No. 6610836
GENRAL INFORMATION:
FOR TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PIREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3698
LENGTH: 1245
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Sequence 3, Application US/08725758A

Sequence 3, Application US/08725758A

Patent No. 6160108

GENERAL INFORMATION:
APPLICANT: Reed, Guy
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Clement, Christophe Y.
APPLICANT: Tish & Ichardson P.C.
STREET: 225 Franklin Street
COUNTRY: USA

ZIP: OUNTRY: USA
ZIP: OUNTRY: LBM Compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DISKETEN: OSPITMANE: FASCESQ Version 2.0
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Length 1373;
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Patent No. 663968

GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glocate, S.
TITLE OF INPORTION: BSTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 788

LENGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.6%; Score 16.2; I Best Local Similarity 85.7%; Pred. No. 83; Matches 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                     372 raadadatrcceeerer 389
                                                                                                                                                                                    74.5%;
94.4%;
                                                                                                        Coding Sequence
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASESED for Win
                                                                                                                                                                                    Query Match
Best Local Similarity 94.4
Matches 17; Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                    linear
                                              TOPOLOGY: 11
MOLECULE TYPE:
                           STRANDEDNESS:
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                                                                                   ; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-725-758A-1
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ZIP: 94304
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; LOCATION: 306
US-09-621-976-788
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Parent No. 6166108
GENERAL INFORMATION:
APPLICANT: Reed, GUY
APPLICANT: Clement, Christophe Y.
TITLE OF INVENTION: NOVEL PLATELET ACTIVATION PROTEIN
NUMBER OF SEQUENCES: 4
CORRESSEDENDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.4; DB
Pred. No. 71;
0; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,758A
FILING DATE: 04-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,074
FILING DATE: 06-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: FEASE, Jahis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/020001
TELECOMMULICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 0517-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTESCO VERSION 2.0
SURENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 04-0CT-1996
PRICK APPLICATION DATA:
APPLICATION NUMBER: 60/005,074
FILING DATE: 06-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: FEASEY, Janis K.
REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 05433/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
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                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1273 base pairs TYPE: mucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KBY: Coding Sequence;
LOCATION: 44...1273
US-08-725-758A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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IBM Compatible
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MEDIUM TYPE: Diskett
COMPUTER: IBM COMDAT
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA
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STREET: Zer.
TTY: Boston
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US-08-725-758A-1
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Score 16.2; Di
Pred. No. 96;
0; Mismatches
                                                                                                                                                                                                                                     S-09-313-294A-5461/c
Sequence 5461, Application US/09313294A
Parent No. 6476212
GENERAL INFORMATION:
                                                                                                                                                       2401 TGAGTGAGTTTTGGATGTCCT 2421
                                                                                                               1 TGAGAGAGTTCTGGGTGTCCT 21
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                            Query Match
Best Local Similarity 85.7%;
Matches 18; Conservative
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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LENGTH: 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
ATPORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RESTERRATION NUMBER: 36,749
RESTERRATION NUMBER: 36,749
RESTERRATION NUMBER: 36,749
RESTERRATION NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: CONIE, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                 ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION WINDRER: 36,749
REFERENCE FOOCKET NUMBER: 36,749
REFERENCE FOOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Patent No. 6300472
                                                                                                                                                                                                                                                                                                            LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Palo Alto
STATE: CA
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-313-294A-4815/c

US-09-313-294A-4815/c

Sequence 4815 Application US/09313294A

Sequence 4815 Application

Sequence 4815 Application

Sequence 4815 Application

GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Brains Brailey

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

FILE REFERENCE: PL-0017 US

CURRENT APPLICATION NUMBER: US/09/313,294A

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PPRL PROGRAM

SEQ ID NO 4815

LENGTH: 283
                                                            Gaps
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DB 4; Length 2713;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700350185H1
US-09-313-294A-5461
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CTHER INFORMATION: Incyte ID No. 6476212 700349077H1
NAME/KEY: unsure
LOCATION: 14, 132
COTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4815
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Sequence 5, Application US/09653839
Patent No. 6433153
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        755 AGACAGTTCTGGTTGTCCT 773
                                                                                                                                                                                                                                                                                                                                                                                                               3 AGAGAGTICIGGGIGICCT 21
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Homo sapiens
US-09-833-381-1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-653-839-5
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US-09-653-839-7
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US-09-313-294A-2911/C
US-09-313-294A-2911/C
); Sequence 2911, Application US/09313294A
); Patent No. 6476212
); GENERAL INFORMATION:
); APPLICANT: Lalgudi, Raghunath V.
); APPLICANT: Lalgudi, Raghunath V.
); APPLICANT: Bradley K.
); TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
); FILE REPERBNCE: PL-0017 US
); CURRENT PILING DATE: 1999-05-14
); NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL PROGRAM
                                                                                                                                                                          APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPRESENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 809
LENGTH: 288
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.8%; Score 15.8; DB 4; Length 288;
89.5%; Pred. No. 1.2e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549871H1
US-09-313-294A-809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700553476H1
US-09-313-294A-2911
                                                                                    RESULT 9
US-09-313-294A-809/c
; Sequence 809, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-833-381-1328
; Sequence 1328, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
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1 TGAGAGAGTTCTGGGTGTC 19
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
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## APPLICANT: Dunoho, Gregory
## APPLICANT: Dunoho, Gregory
## APPLICANT: Turner, C. Alexander Jr.
## APPLICANT: Turner, C. Alexander Jr.
## APPLICANT: Friedrich, Glenn
## APPLICANT: Sambrowicz Brian
## APPLICANT: Sambrowicz Brian
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## APPLICANT: Sambrowicz Brian
## APPLICANT: Sam
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APPLICANT: Robison, Keith E.

TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1328
LENGTH: 835
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Pred. No. 1.3e+02;
0; Mismatches 2; Indels
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APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Tarner, Glenn
APPLICANT: Sands Arthur T.
TITLE OF INVENTION: and Polymucleotides Encoding the Same
TITLE OF INVENTION: and Polymucleotides Encoding the Same
CURRENT APPLICATION NUMBER: US/09/653,839
CURRENT APPLICATION NUMBER: US 60/152,057
PRIOR PILICATION NUMBER: US 60/152,057
PRIOR PILICATION NUMBER: US 60/152,057
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09653839
Fatent No. 6433153
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Priedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arrhur T.
TITLE OF INVENTION: and Polynucleotides Encoding the Same
TITLE OF INVENTION: and Polynucleotides Encoding the Same
TITLE OF INVENTION: US/09/653,839
CURRENT FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                         Score 15.8; DB 4;
Pred. No. 1.4e+02;
0; Mismatches 2;
CURRENT APPLICATION NUMBER: US/09/653,839
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,057
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 2109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1067 decadircrecardrecta 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                    956 GGGAGTTCTGGATGTCCTA 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09653839
Patent No. 6433153
                                                                                                                                                                                                                                                                                                                                                                                                          4 GAGAGTTCTGGGTGTCCTA 22
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.53
Matches 17; Conservative
                                                                                                                                                                                                     TYPE: DNA
ORGANISM: homo sapiens
US-09-653-839-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: homo sapiens US-09-653-839-3
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## PRIOR FILING DATE: 1999-09-02

| WUNDER OF SEQ ID NOS: 9
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 1
| LENGTH: 2220
| TYPE: DAS |
| ORGANISM: home sapiens |
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JS-09-814-353-21302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21302, A Sequence 953, App Sequence 1362, App Sequence 35, App Sequence 224, Appl Sequence 131512, Sequence 131512, Sequence 39447, A Sequence 23260, A Sequence 11, Appl Sequence 11, Appl
                                                                                                                         February 19, 2004, 23:23:34; Search time 52.8809 Seconds (without alignments) 1456.787 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA:*

1: \cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: \cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: \cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: \cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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11: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
12: \cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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18: \cgn2_6/ptodata/2/pubpna/US10A_PUB.seq:*
18: \cgn2_6/ptodata/2/pubpna/US10A_PUB.Seq:*
18: \cgn2_6/ptodata/2/pubpna/US10A_PUB.Seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-108-260A-1362

US-10-108-260A-1362

US-10-108-563-36

5 US-10-108-563-36

5 US-10-027-632-131511

5 US-10-027-632-131512

10S-10-282-122A-37180

2 US-10-282-122A-3998

2 US-10-282-122A-39447

5 US-10-282-122A-3260

5 US-10-428-487-11
                                                                                                                                                                                                                                                                                                                                                                                                               lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                            2308684 seqs, 1750822206 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                1 tgagagttctgggtgtccta 22
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10:0 , Gapext 1.0
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22
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                            Searched:
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                                                                                                                           Run on:
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No.
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## ALIGNMENTS

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APPLICANT: Billy X. Asonong
APPLICANT: Billy X. Asonong
APPLICANT: Billy X. Asonong
APPLICANT: Ball Alease
APPLICANT: Gerlaen, Valerie
APPLICANT: Gerlaen, Billy Alease
APPLICANT: Schusen, Bryan D
ITTLE OF INVERTION: Using the Same
FILE REPERBNCE: 12402-279
FILE OF INVERTION: Using the Same
CURRENT PAPLICANTON NUMBER: US/10/080,334
CURRENT PILLNO DATE: 2001-02-20
PRIOR PELICATION NUMBER: 60/320,77
PRIOR APPLICATION NUMBER: 60/320,77
PRIOR APPLICATION NUMBER: 60/320,70
PRIOR APPLICATION NUMBER: 60/270,520
PRIOR APPLICATION NUMBER: 60/270,520
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PRIOR PLING DATE: 2001-08-10
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Pred. No. 64;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patturajan, Meera
Gangolli, Esha A
Padigaru, Muralidhara
Liu, Xiaohong
      i No. US20040002584Al
ORMATION:
Pena, Carol E. A.
Shimkets, Richard A
                                                                                                                                                                                                                    Spytek, Kimberly A
Vernet, Corine A. M
Malyankar, Uriel M
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chernev, Velizar
                                                                                                                                                                                                                                                                                                                                                                    Casman, Stacie J
Boldog, Ferenc L
Furtak, Katarzyna
                                                                                                                                   Li, Li
Shenoy, Suresh G
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                           Gusev, Vladimir Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-080-334-85
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Frad,
APPLICANT: Mehraban, Frad,
APPLICANT: Mehraban, Frad,
APPLICANT: Conley, Pamela
APPLICANT: Donley, Pamela
APPLICANT: Topper, James
APPLICANT: Topper, James
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APPLICANT: Topper, James
APPLICANT: Mon. USC0020082206Alel Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: USSN 60/208,427
PRIOR APPLICANTION NUMBER: USSN 60/208,427
PRIOR APPLICANTION NUMBER: USSN 60/208,427
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
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      DB 10; Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 92.7%; Score 20.4; DB 9; Length 763; Best Local Similarity 95.5%; Pred. No. 2.1; Matches 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WS-10-108-260A-1362/c
| Sequence 1362, Application US/10108260A
| Publication No. US20040005560A1
| GENERAL INFORMATION:
| APPLICANT: HELIX RESEARCH INSTITUTE
| TILLE OF INVENTION: No. US20040005560A1e1 full length cDNA
| FILE REFERENCE: H1-A0106
| CURRENT APPLICATION NUMBER: US/10/108,260A
| CURRENT PILION DAIR: 2002-03-27
| NUMBER OF SEQ ID NOS: 5458
| SOFFWARE: PAFCENTIN Ver. 2.1
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Query Match
100.0%; Score 22; DB 10
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Pred. No. 41
                                                                                                                                                                          276 TGAGAGTTCTGGGTGTCCTA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 readadarricredardrecra 133
                                                                                                                                                                                                                                                                                                                                 ; Sequence 953, Application US/03867550; Patent No. US20020082206A1; GENERAL INFORMATION:
                                                                                                                          1 TGAGAGATTCTGGGTGTCCTA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGAGAGATTCTGGGTGTCCTA 22
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US-10-080-334-85
; Sequence 85, Application US/10080334
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Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-867-550-953
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; ORGANISM: Homo sapiens
US-10-108-260A-1362
                                                                                                                                                                                                                                                                       RESULT 2
US-09-867-550-953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1362
LENGTH: 2064
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LENGTH: 763
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Gaps

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GENERAL INCURRATION:

GENERAL INCURRATION:

APPLICANT:
Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/27,632

CURRENT APPLICATION NUMBER: US/00.74.30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/198,218

PRIOR APPLICATION NUMBER: US 60/186,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastesQ for Windows Version 4.0

LENGTH: 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2789;
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                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030232349A1 5155802CB1
US-10-274-639-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.1%; Score 17.4; DB 15; Best Local Similarity 94.7%; Pred. No. 64; Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.2%; Score 17.2; DB 15;
86.4%; Pred. No. 79;
ive 0; Mismatches 3;
PRIOR APPLICATION NUMBER: US 60/224,717
PRIOR FILING DATE: 2000-08-11
PRIOR PELLING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 42
SOFWARE: PERL PROGRAM
LENGTH: 2789
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; Sequence 284738 Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
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; Sequence 111511, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 readacarrrcreedrercara 217
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Best Local Similarity 86.45
Matches 19; Conservative
                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Human
US-10-027-632-284738
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                                                                                                                                                                                                                                                                       APPLICANT: Kian, Javed
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
FILE REFERENCE: 11613.56US11
CURRENT PELING DATE: 2002-12-09
PRIOR PELICATION NUMBER: US/10/159,563
PRIOR APPLICATION NUMBER: US/10/133,937
PRIOR RILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SEQ ID NO 396
LENGTH: 2466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15; Length 2466;
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APPLICANT: DELEGERANE, Angelo M.; GANDHI, Ameena R.
APPLICANT: DELEGERANE, Angelo M.; GANDHI, Ameena R.
APPLICANT: HAFALIA, April J.A.; LU, Dyung Aina M.
APPLICANT: DAS, Debopriya; KALIZCK, Deborah A.
APPLICANT: NGUYEN, Danniel B.; LEE, Ernestine A.
APPLICANT: NGUYEN, Danniel B.; LEE, Ernestine A.
APPLICANT: AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.
APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi APPLICANT: BURFORD, Nail; KEARNEY, Liam
APPLICANT: BURFORD, Nail; WALIA, Narinder K.
APPLICANT: JOHO, Stephen; LO, Terence P.
APPLICANT: TODD, Stephen; LO, Terence P.
APPLICANT: TODD, Stephen; LO, Terence P.
APPLICANT: TANG, Y. Tom; ELLIOTT, VICKI S.
APPLICANT: ALLO, PROTEASES
FILE REFERENCE: PI-O167 USA
CURRENT APPLICANTON: PROTEASES
FILE REFERENCE: PI-O167 USA
CURRENT APPLICATION NUMBER: US/10/274,639
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0; Mismatches
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PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/220,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/220,063
FILING DATE: 2000-07-21
APPLICATION NUMBER: US 60/221,680
APPLICATION NUMBER: US 60/221,680
APPLICATION NUMBER: US 60/223,544
FILING DATE: 2000-08-04
                                                                                                                                                                                               Sequence 396, Application US/10159563
Publication No. US20040009154A1
GENERAL INFORMATION:
                                         1116 GAGAGTTCTGGATGTCCTA 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/10274639
Publication No. US20030232349A1
GENERAL INFORMATION:
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US-10-159-563-396
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Best Local Similarity
Matches 18; Conserv
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Best Local Similarity 86.4%;
Matches 19; Conservative
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wall, Da
Trawick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-282-122A-38988
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Sequence 131512, Application US/10027632

Publication No. US203020407539

FUBLICATION: US203020407539

FUBLICATION: US203020407539

FUBLICATION: US203020407539

FILTE OF INVENTION: POLYMORPHISMS in the Human Genome

FILE OF INVENTION: POLYMORPHISMS in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

FRIOR PELICATION NUMBER: US 60/218,006

FRIOR PELICATION NUMBER: US 60/193,483

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-10-28

FRIOR FILING DATE: 1999-108-09

FRIOR FILING DATE: 1999-08-09

FRIOR FILING DATE: 1999-08-09

FRIOR FILING DATE: 1999-08-09

FRIOR FILING DATE: 1999-08-09

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      Wang, David G.
NVENTION: Identification and Mapping of Single Nucleotide
NVENTION: Polymorphisms in the Human Genome
ENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 641;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mappi
FILE REFERENCE: 108627.129
CURRENT PAPLICATION NUMBER: US,10/027,632
CURRENT PILLING DATE: 2002-04-30
PRIOR PELLING DATE: 2000-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PLING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131511
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Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.4
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-131511
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US-10-027-632-131512
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ORGANISM: Human
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TION: Identification of Essential Genes in Microorganisms
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Application data removed - See File Wrapper or PALM
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Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60,191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PELLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-09-06
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
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PRIOR PELLING DATE: 2000-12-27
PRIOR PELLING DATE: 2000-12-27
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
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PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
Sequence 37180, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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US-10-282-122A-23260
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT ELING DATE: 2003-02-20
PRIOR PILICA DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FLE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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86.4%; Pred. No. 80;
live 0; Mismatches 3;
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PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Salmonella typhimurium
US-10-282-122A-38988
                                                                                                                  Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
Robert
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                         skind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.4<sup>3</sup>
Matches 19; Conservative
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms CURRENT EDITES. 2014.

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/291,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PLING DATE: 2000-05-23
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78.2%; Score 17.2; D.
Best Local Similarity 86.4%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches
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Publication No. US20040029129A1
GENERAL INFORMATION
APPLICANT: Wang, Liangsu
APPLICANT: Aamudio, Carlos
APPLICANT: Hacelbeck, Robert
APPLICANT: Hacelbeck, Robert
APPLICANT: Ohisen, Kari
APPLICANT: Zyskind, Judith
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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PRIOR APPLICATION UNBER: 60/201,335
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Salmonella typhi
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| Sequence 11, Application US/10428487 |
| Publication No. US20040006780A1 |
| GENERAL INFORMATION: US20040006780A1 |
| APPLICANT: RASTELLI, LUCA K. |
| APPLICANT: GENERE, HANS-PETER |
| TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM |
| FILE REFERENCE: 09800080-0103 |
| CUTRENT APPLICATION NUMBER: US/10/428,487 |
| CURRENT PILING DATE: 2003-05-02 |
| PRIOR FILING DATE: 2001-03-21 |
| PRIOR FILING DATE: 2001-03-22 |
| NUMBER OF SEQ ID NOS: 84 |
| SEQ ID NO 11 |
| LENGTH 2003-10 |
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PRIOR FILING DATE: 2000-12-24
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SCPTWARE: Patentin version 3.1
SEQ ID NO 23260
LENGTH: 1185
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Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA

FILE REFRENCE: H1-A015

CURRENT APPLICATION NUMBER: US/10/104,047

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1043

LENGTH: 2394
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Pred. No. 80;
0; Mismatches 3;
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CRGANISM: Klebsiella pneumoniae
US-10-282-122A-23260
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Best Local Similarity 86.4%;
Matches 19; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                       Length 301692;
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76.4%; Score 16.8; DB 15;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                   Search completed: February 20, 2004, 05:59:27 Job time : 59.8809 secs
                                                                                                                                                                      69276 AGAGATTGCTGGGTGTCCTA 69257
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US-10-428-487-11
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